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OM protein - protein search, using sw model

Run on: March 27, 2005, 20:32:06 ; Search time 54 Seconds
(without alignments)
1118.354 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVKNKVPIGENNEN.....PSAEGGEVLTVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pgp:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pgp:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pgp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3166.5	74.8	610	4	US-09-949-016-6945
2	2202	52.0	416	4	US-09-949-016-11669
3	1949	46.0	909	4	US-09-538-092-1315
4	857	20.2	698	4	US-09-949-016-10215
5	850	20.1	694	4	US-09-538-092-1351
6	818.5	19.3	690	4	US-09-275-252A-19
7	817	19.3	686	4	US-09-538-092-1037
8	817	19.3	694	4	US-09-949-016-11549
9	484	11.4	261	4	US-09-275-252A-18
10	416.5	9.8	256	4	US-09-270-767-46624
11	413	9.8	1203	4	US-09-949-016-6615
12	412.5	9.7	910	4	US-08-997-685A-6
13	412.5	9.7	910	4	US-09-086-436-31
14	412.5	9.7	1109	4	US-09-949-016-10771
15	405.5	9.6	889	4	US-09-949-016-6036
16	399.5	9.4	855	4	US-09-949-016-7263
17	382.5	9.0	749	4	US-08-997-685A-10
18	382.5	9.0	749	4	US-09-086-436-39
19	382	9.0	528	4	US-08-997-685A-4
20	377.5	8.9	504	4	US-09-086-436-33
21	370	8.7	597	4	US-08-997-685A-12
22	368	8.7	506	4	US-08-997-685A-6
23	368	8.7	506	4	US-09-086-436-35
24	368	8.7	597	4	US-09-086-436-41
25	360.5	8.5	960	4	US-09-694-777A-21
26	349	8.2	987	4	US-09-694-777A-22
27	347.5	8.2	962	4	US-09-694-777A-24

28	345.5	8.2	962	4	US-09-614-480-9	Sequence 9, Appl
29	345.5	8.2	962	4	US-09-694-777A-3	Sequence 3, Appl
30	345.5	8.2	962	4	US-10-422-0775-9	Sequence 9, Appl
31	344	8.1	170	4	US-09-358-383C-27	Sequence 27, Appl
32	337	8.0	988	4	US-10-162-012-12	Sequence 12, Appl
33	336	7.9	989	4	US-09-694-777A-23	Sequence 23, Appl
34	335	7.9	988	4	US-09-614-480-2	Sequence 2, Appl
35	335	7.9	988	4	US-10-162-012-5	Sequence 5, Appl
36	335	7.9	988	4	US-10-422-075-2	Sequence 2, Appl
37	334	7.9	319	4	US-09-358-383C-22	Sequence 22, Appl
38	334	7.9	989	4	US-09-694-777A-4	Sequence 4, Appl
39	317.5	7.5	1159	2	US-08-956-242-13	Sequence 13, Appl
40	317.5	7.5	1159	3	US-09-351-215-13	Sequence 13, Appl
41	317.5	7.5	1159	3	US-09-226-012-2	Sequence 2, Appl
42	317.5	7.5	1159	3	US-09-226-012-4	Sequence 4, Appl
43	317.5	7.5	1159	4	US-09-358-383C-10	Sequence 10, Appl
44	317.5	7.5	1159	4	US-09-275-252A-12	Sequence 12, Appl
45	302.5	7.1	857	4	US-09-275-252A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-6945
; Sequence 6945, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6945
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6945

Query Match	74.8%	Score	3166.5	DB	4	Length	610
Best Local Similarity	99.0%	Pred. No.	3.5e-273				
Matches	609	Conservative	0	Mismatches	1	Indels	5
Gaps	1						
Qy	195	MLPEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPRLVPPYQADNIHYWL	254				
Db	1	MLPEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPRLVPPYQADNIHYWL	60				
Qy	255	IADIICDIYLYDMLFTQPRLOFVRGGDIIVDSNELKRYHTSTKFDQDASIIPFDICY	314				
Db	61	IADIICDIYLYDMLFTQPRLOFVRGGDIIVDSNELKRYHTSTKFDQDASIIPFDICY	120				
Qy	315	LFPGFNPFRANRMLKYTSFFEFNHLESIMDKAYIRVIRTTGYLLFILHINACVYWA	374				
Db	121	LFPGFNPFRANRMLKYTSFFEFNHLESIMDKAYIRVIRTTGYLLFILHINACVYWA	180				
Qy	375	SNYEGIGTRWVYDGEYRCYVAVRTLITIGGLPEPOTLFEIVFQLLNPFSGVVP	434				
Db	181	SNYEGIGTRWVYDGEYRCYVAVRTLITIGGLPEPOTLFEIVFQLLNPFSGVVP	240				
Qy	435	SSLLGQMRDVTGAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRM	494				
Db	241	SSLLGQMRDVTGAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRM	300				
Qy	495	ESDLLKLTPTTVQLALAIQVNFISIISKVDLPKGCOTQMIYDMLRLKSVLYLPGDFVCK	554				

; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1037
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(6)
; OTHER INFORMATION: Polypeptide Accession Number P29973
US-09-538-092-1037

Query Match 19.3%; Score 817; DB 4; Length 686;
Best Local Similarity 29.9%; Pred. No. 9.2e-64;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

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QY 5 LTKNVKVPICGENNENEGSSRRNEEGSHPS-----NQSQTTAQENKGE-----KSL 53
DB 13 VTMPNVIVP-----DIEKEIRRMENGACSSFSDEDDSDASTSESEENPHARGSFYSKSL 67
QY 54 KTKSTPTVTSBPHNTIQDKLSKNSGDLTTPDQNAAEPTGTVPQEKMDPGKEGNS 113
DB 68 R-KGSPSQREQLPGALFNVNNS-----NKD-----QEPEKKKKKKKSKSDDKNE 117
QY 114 POKPPAAPVINEYADAQLHNLVKRMQRTALYKKLVEGDLSSPEASPTAKPTAVPPV 173
DB 118 NKNDPE-----KSKKKKKKKKK-----E 137
QY 174 KESDDKTEHYRLLWPKVKKMPLETKRIKLPNSIDSYDRLYLMLLVTL--AYNW 231
DB 138 ESKDKKEE-----KKEVV-----IDP-SGNTYYNWLFCITLPMVYNW 176
QY 232 NCWFPIRLVPYQADNIHMYLIADIIICDIYLYDMLFIQPLQFVRGGDIIVDSNELR 291
DB 177 T--WVIARACFDELQSDVLEWLLDYVSDIVYLDM-FVTRTGYLEQGLLVKEELKLI 233
QY 292 KHYRTSTKQOLDVASIIPFDICYLFFGN-PMFRANRLKYSFPEFNHLESIMDKAYI 350
DB 234 NKYSNLQFKLDVLSLITDLYLPGKLGWNYPEIRLRLFRSMPFQRTETRTNYNI 293
QY 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWY-----DGE-----GNEYLRCCYVAV 402
DB 294 FRISNLVWYVIIHWNACVYSISKAIGFNGDWTWVPDINDPEFGRILARKYVYSLYWS 353
QY 403 RLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQMDRVIGAAATANQYFRACMDDT 462
DB 354 LTLTIGTTPPPVRDSEVVFVVDLGLVLFATIVGNIGSMISNMNARAFAQARIDAI 413
QY 463 IAYMNNYSIPKLQKRVRTWYEYTDWSQRLMDESLLKTLPTTVOLALAIIVNFSISKV 522
DB 414 KQYMHFRNVSKDMKRVIKWFDYLTWNTKKTVEKLVKLPDKLRAEIAINVHLDLTKV 473
QY 523 DLFGCDTQMYDMLRLKSVLYLPDGFVCKKGIGKEMWYIIKHGEVOLVGGPQTKVLV 582
DB 474 RIFADCEAGLVELVQLQVYSPGDIYCKKGIGREMYIIKEGKLVV-ADGVTQFV 532
QY 583 TLKAGSVFGEISLLAAGS---GNRTANVVAHGFANLLTLDKKTLOEILVHYPPSERILM 639
DB 533 VLSGYSYFGEISILNIGSKAGNRRTANIKSIGYSDLFCLSKDDLMALTEYPPDAKTMLE 592
QY 640 KKAUVLLKQKA-----KTAEBATPPPKOLALLPPPKETPKLTKLGGTGKASLARLL--- 692
DB 593 EKGQILMKDGLDLNLANAGSDPKDLEEKVTRMEGSDVLLQT-----RFAILAEY 644
QY 693 -----KLRGAAOKK-----ENSEG-GBEEG 713
DB 645 ESMQKQLKRLTKVEKFLKPLIDTEFSSIEGPGAESG 681
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RESULT 8

US-09-949-016-11549

; Sequence 11549, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 11549
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11549

Query Match 19.3%; Score 817; DB 4; Length 694;
Best Local Similarity 29.9%; Pred. No. 9.4e-64;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

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QY 5 LTKNVKVPICGENNENEGSSRRNEEGSHPS-----NQSQTTAQENKGE-----KSL 53
DB 21 VTMPNVIVP-----DIEKEIRRMENGACSSFSDEDDSDASTSESEENPHARGSFYSKSL 75
QY 54 KTKSTPTVTSBPHNTIQDKLSKNSGDLTTPDQNAAEPTGTVPQEKMDPGKEGNS 113
DB 76 R-KGSPSQREQLPGALFNVNNS-----NKD-----QEPEKKKKKKKSKSDDKNE 125
QY 114 POKPPAAPVINEYADAQLHNLVKRMQRTALYKKLVEGDLSSPEASPTAKPTAVPPV 173
DB 126 NKNDPE-----KSKKKKKKKKK-----E 145
QY 174 KESDDKTEHYRLLWPKVKKMPLETKRIKLPNSIDSYDRLYLMLLVTL--AYNW 231
DB 146 ESKDKKEE-----KKEVV-----IDP-SGNTYYNWLFCITLPMVYNW 184
QY 232 NCWFPIRLVPYQADNIHMYLIADIIICDIYLYDMLFIQPLQFVRGGDIIVDSNELR 291
DB 185 T--WVIARACFDELQSDVLEWLLDYVSDIVYLDM-FVTRTGYLEQGLLVKEELKLI 241
QY 292 KHYRTSTKQOLDVASIIPFDICYLFFGN-PMFRANRLKYSFPEFNHLESIMDKAYI 350
DB 242 NKYSNLQFKLDVLSLITDLYLPGKLGWNYPEIRLRLFRSMPFQRTETRTNYNI 301
QY 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWY-----DGE-----GNEYLRCCYVAV 402
DB 302 FRISNLVWYVIIHWNACVYSISKAIGFNGDWTWVPDINDPEFGRILARKYVYSLYWS 361
QY 403 RLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQMDRVIGAAATANQYFRACMDDT 462
DB 362 LTLTIGTTPPPVRDSEVVFVVDLGLVLFATIVGNIGSMISNMNARAFAQARIDAI 421
QY 463 IAYMNNYSIPKLQKRVRTWYEYTDWSQRLMDESLLKTLPTTVOLALAIIVNFSISKV 522
DB 422 KQYMHFRNVSKDMKRVIKWFDYLTWNTKKTVEKLVKLPDKLRAEIAINVHLDLTKV 481
QY 523 DLFGCDTQMYDMLRLKSVLYLPDGFVCKKGIGKEMWYIIKHGEVOLVGGPQTKVLV 582
DB 482 RIFADCEAGLVELVQLQVYSPGDIYCKKGIGREMYIIKEGKLVV-ADGVTQFV 540
QY 583 TLKAGSVFGEISLLAAGS---GNRTANVVAHGFANLLTLDKKTLOEILVHYPPSERILM 639
DB 541 VLSGYSYFGEISILNIGSKAGNRRTANIKSIGYSDLFCLSKDDLMALTEYPPDAKTMLE 600
QY 640 KKAUVLLKQKA-----KTAEBATPPPKOLALLPPPKETPKLTKLGGTGKASLARLL--- 692
DB 601 EKGQILMKDGLDLNLANAGSDPKDLEEKVTRMEGSDVLLQT-----RFAILAEY 652
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; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46624

Query Match          9.8%; Score 416.5; DB 4; Length 256;
Best Local Similarity 36.8%; Pred. No. 9.6e-29;
Matches 78; Conservative 53; Mismatches 80; Indels 1; Gaps 1;

Qy 253 WLADIICDIYLYDMLFIQPRQLQFVRGGDIIVDSNELRKHVRTSTKTKOLDVASIIPDI 312
Db 45 WLACDFCADIYLLDVVFFKRVVYLFEGFVWKNKLNTRKNYMRKLQFKLDLALLPLEL 104

Qy 313 CYLFFGFNPMF-RANRMLKYTSFFRNHLSIMDKAYIVRITTYGLLFTLHNACVY 371
Db 105 LYFKLGTQAVLWRFPFFKIQSFWEVFRLLDRVISDPHVRVAKLTWLYMIHTAALY 164

Qy 372 YWASNYEGIGTRWVYDGEENEYLCYYWAVRTLITIGLPEPQTLFEIVFOLLNFFSGV 431
Db 165 YAYS DYQGLGNRWVFSKGHPVRCFAFATKTATSIGNPKPQEQGYETVMTVAWLMGV 224

Qy 432 FVFSSLIQMRDVIGATATQNYFRACMDTI 463
Db 225 FVFALLIGIRDIISTATRNKHEYROLEDTL 256

RESULT 11
US-09-949-016-6615
; Sequence 6615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6615
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6615

Query Match          9.8%; Score 413; DB 4; Length 1203;
Best Local Similarity 23.9%; Pred. No. 2.2e-27;
Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

Qy 62 SERPHNIQDKLSKKN--SSGDLTTNPD---PQNAAEPTGTVPQEKMDPGKE-----GP 111
Db 115 SGSSHGHLDHSAEERLIAGDSAPGEDRTPPGLAAEPE-----RPGSAAQPAASP 165

Qy 112 NSPQNKPPAAPVINEYADALHNLVVRMRQRTAL-YKKKLVEGDSGPSASQPTAKPTAV 170
Db 166 PPOQPPQPPASACEQPSVD-----TAIKVEGGAAGADQILPEAEVRLGQAGFM 214

Qy 171 PPVKESDDKPEHYHYRLLMFKVKKMPLETVLKEIKLPN--SDSYTD-RLYLLWLLLVTL 227
Db 215 QROFGAMLOQGVNKFSLRMFGSQKAVEREQ-ERKVSAGFWIHPYSDFRFY--WDLTMLL 271

Qy 228 AYNNWCWFIFLRVLPFYQYADNIHYWLIADIIICDIYLYDMLFIQPRQLQFVRG-----G 281
Db 272 LMVGNLIIIPVGITF--FKDENTTPWIVFNVDSTFFLIDLV-----LNFRTGIVVEDNT 324

Qy 282 DIIVDSNELRKHVRTSTKTKOLDVASIIPDICYL-----PFGFNPMF 323
Db 282 DIIVDSNELRKHVRTSTKTKOLDVASIIPDICYL-----PFGFNPMF 323

; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match          11.4%; Score 484; DB 4; Length 261;
Best Local Similarity 37.2%; Pred. No. 9.6e-35;
Matches 97; Conservative 58; Mismatches 94; Indels 12; Gaps 4;

Qy 370 VYWASNYEGIGTRWVY----DGE-----GNEYLRCYYWAVRTLITIGLPEPQTLFEIV 421
Db 1 IYVAISKISIGFVDTWVYNNITDPXYGLAREVIYCLYWSTLTITIGETPPPVKDESVL 60

Qy 422 FOLLNPFSGVVFSSLIQMRDVIGATATQNYFRACMDTIAYNNVYISPKLVOKRVRT 481
Db 61 FVIFDFLIGVLPATIVGNVGMISNNATRAEFQAKIDAVKHYMQFRKVSXGMEAKVIR 120

Qy 482 WYETWDSQRMLESLLKTLPTVOLALADVNPESIISKVDLEKGCDDTOMIYDMLRLK 541
Db 121 WFDYLTNKTVDEREITLKNLPAKRAETAINVHLSTLKKVRFHPDCEAGLLVELVKLR 180

Qy 542 SVLYLPDGFVCKKGEIKEMYYIKHGEVOVLGGPDGTVLTKAGSVEGEISLAAAG- 600
Db 181 PQVFSFGDYICRKGDIKEMYYIKHGEVLA--ADDGVTQVALLSAGSCFGEISILNKG 239

Qy 601 --GNRTANVVAHGFANLTL 619
Db 240 KMGNNRTANIRSLGYSDFLCL 260

RESULT 10
US-09-270-767-46624
; Sequence 46624, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46624
; LENGTH: 256
; TYPE: PRT

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Db 325 EILDPQRIKMYLXSW-FMVDFTISSIPVDYIFLIVETRIDSEVYKTBARALRIVRFTKIL 383
Qy 324 RANRLKYTSFFEFNHLESIMDKAY-----IYRVIRTTGYLLFLFHINACVYVWASNYE 378
Db 384 SLRLRLRLIRYIHOWEEIFHMTYDLASAVRIVNLIGMMLLCHWDGCLQFLVPMQLQ 443
Qy 379 GIGTRW-----VYDGGNEYLRCYYWAVRLLTIG-GLPEPQTLFEIVFOLLNFFPGV 431
Db 444 DFPDCCWVSINNWNNSGKQSYALFRAMGHMLCIGYGROAPVGMGSDVWLTMLSMIVGA 503
Qy 432 FVFGSLIGMRDVI GAATANQYPRACMDDTIAYNNYSIPKLQKRVRTWVEYTDWSQR 491
Db 504 TCYAMFICHATALIOSLSSRRQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 562
Qy 492 MLDESLLKTLPTTVQLALADVNFS-----IISKVDLFGCDTQMIYDMLRLKSLVLYLP 548
Db 563 MFDEESILGELSEPLREEI---INFNCRKLVASMEFLFANADPNFVTSMLTKLRPEVFPQ 619
Qy 549 DFCVCKGGEIGEMWYIHKGEVQVL-GGPDGTGKVLVTLKAGSVFGEISLLAAGGNRRTPAN 607
Db 620 DYIIREGTIGKMYFIQHVSVLTGKNKTK----LADGSYFGEICILLTRG---RRTAS 672
Qy 608 VVAHGFANLLTKDKTLOEILVHVYDPDSERILMKKA 642
Db 673 VRADTYCRLYSLSDNFNEVLEEYP-----WMRRA 702

RESULT 12

US-08-997-685A-2
; Sequence 2, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997.685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

LENGTH: 910

TYPE: PRT

ORGANISM: mouse

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (130)..(148)

OTHER INFORMATION: S1

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (164)..(185)

OTHER INFORMATION: S2

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (208)..(229)

OTHER INFORMATION: S3

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (243)..(271)

OTHER INFORMATION: S4

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (291)..(313)

OTHER INFORMATION: S5

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (332)..(358)

OTHER INFORMATION: P

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (367)..(387)

OTHER INFORMATION: S6

FEATURE:

; NAME/KEY: DOMAIN
; LOCATION: (472)..(602)
; OTHER INFORMATION: CNB
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC53518
; DATABASE ENTRY DATE: 1997-12-27
; RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2

Query Match

9.7%; Score 412.5; DB 4; Length 910;

Best Local Similarity 20.2%; Pred. No. 1.6e-27;

Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;

Qy 210 IDSYTD-RLYLLMLLLVTLAYNNWCWFIPLRLVFPYQYADNIHNLWLIADIICDIYLYDM 268
Db 124 IHPYSDFRFY--WDLIMLMVGNLVIIPVGITE--FTEQTTTPWIFNVASDTVFLDL 179
Qy 269 LFIQPRLOFVRG-----GDIIIVDSNELRKHRYSTKFDLDVASIIPDICYL----- 315
Db 180 I-----MNFRTGTVNESSEIILDPKVIKMYLXSW-FVVDFTISSIPVDYIFLIVEGMD 233
Qy 316 -----FFGFNPMFRANRLKVTSPPEFNHLESIMDKAY-----IYRVIRTTGY 359
Db 234 SEVYKTBARALRIVRFTKILSLRLRLSLRLRYIHOWEEIFHMTYDLASAVRIFNLIGM 293
Qy 360 LLFILHINACVY-----WASNYBEGIGTRWVYDGGNEYLRCYVAVRVLIT 407
Db 294 MLLCHWDGCLQFLVPLQLQDFPPDCWVSLNE-----WVNDSWGKQSYALFKAMSHMLC 347
Qy 408 IG-GLPEPQTLFEIVFOLLNFFSGVVFSSLIQMRDVGATANTQNYPRACMDDTIAYM 466
Db 348 IGYGAQAPVMSDLWITMLSMIVGATCYAMFVGHATALIOSLSSRRQYQYQYQYQYQY 407
Qy 467 NNYGISPKLVQKRVRTWVEYTDWSORMLDESLLKTLPTTVQLALADVNFS---IISKVD 523
Db 408 SFHLKPADMRQKHIDYEHRYQG-KIFDEENILSELNDPLREEI---VNFNCRKLIVATMP 463
Qy 524 LFGCDTQMIYDMLRLKSLVLYLPFGDFVCKKGEIGEMWYIHKGEVQVLGPGDGTGKVLVT 583
Db 464 LFANADPNFVTAMLSKLRFVFPQDYIIREGAVGKMYFIQHVAGVI-----TKSSKE 518
Qy 584 LKA--GSVFGHEISLLAAGGNRRTPANVVAHGFANLLTKDKTLOEILVHVYDPDSER----- 636
Db 519 MKLTDGSYFGEICILLTRG---RRTASVRADTYCRLYSLSDNFNEVLEEYPMRRAPETV 575
Qy 637 -----ILMEK-----ARVLLKQKAK----- 651
Db 576 AIDRLDRIGKNSILQKQKDLNTGVNQNQENELKQIVKHDREMVAQIIPPINYPQMTA 635
Qy 652 ---TAEATPPRKOL-----ALLFP-----P 668
Db 636 LNCITSSITTPISRMRQTSPVYVYATSLSHSNLHSPSPSTQTPQPSAILSPCSYTTAVCSP 695
Qy 669 KBETPKLFTLLGGTGKASLARLLKLKREQAQ---KKENSEGEGEEKENEDKOKENED 725
Db 696 PIQSPLATRTFHVASPTASQLSLMQPQQQLPQSQVQQTQTQTQQQQQQQQQQQQQQQQ 755
Qy 726 KOKENEDKGENEDKDKGREPEEKPLDRPECTASPIAVEEHPHVRVRLPRGTSGRSL- 784
Db 756 QQQ 815
Qy 785 -----IISMAFSAEGEGEVLTI 801
Db 816 HEVSTLIS-RPHPTVGSLSASI 836

RESULT 13

US-09-086-436-31
; Sequence 31, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina

```

; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Murine
US-09-086-436-31

Query Match          9.7%; Score 412.5; DB 4; Length 910;
Best Local Similarity 20.2%; Pred. No. 1.6e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;

Qy 210 IDS YTD-RLYLLWLLVTLANNWCWPIPLRLVFPYOTADNIHNLWLIADIIICDIYLYDM 268
Db 124 IHPYSDFRY--WDLIMLMVGNLVIIIPVGITF--FTEQTTTPWIIIFNVASDTVFLLDL 179

Qy 269 LFIQPRLOQVRG-----GDIIVDSNELKHYRTSTKFDLDVASIIPFDICYL----- 315
Db 180 I-----WNFRIGTVNEDSSSEILLDPKVIKNYLKSW-FVVDFFISSIPVDVIFILVEKGMD 233

Qy 316 -----FFGFNPMFRANMLKYTSPFEFNHLESIMDKAY-----IYRVIRITGY 359
Db 234 SEVYKTARALRIVRFTKILSLRLRLSLRILYTHQWEEIFHMTYDLASAVVRIFNLGM 293

Qy 360 LLFILHINACVY-----WASNYEGITGTWVYDGEVNEVLYRCYYWAVRTLIT 407
Db 294 MLLCHWDGCLQFLVLPQLPDPDCWVSLNE-----MVNDSWKGQSYALFKAMSHMLC 347

Qy 408 IG-GLPEPQTLFEIVFOLLNFFSGVFVFSLLIGOMRDVIGAATANQNYFRACDDTIAYM 466
Db 348 IGYGAQAPVMSDLWITMLSMIVGATCYAMFVGHATALIQSLDSSRRQYQEKYQVEQYM 407

Qy 467 NNTYSIPKLQKRVRTWYETWDSQRMDESLDKTLPTTVQLALADIVNPS-----IISKVD 523
Db 408 SFHKLPADMRQKHIDYEHRYQOG-KIPDEENILSELNDPLREBI--VNFNCRKLVATMP 463

Qy 524 LFKGCDQMTYDMLRLKSLVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPGDGTKVLYT 593
Db 464 LFANADPNFTAMLSKURFEVFGDYIIRREGAVGKKMYFIQHGVAQVI-----TKSKE 518

Qy 584 LKA--GSVFGEISILAAAGGNRRRTANVVAHGFANLLTLDKKTLLQEIIVHYPDSE 636
Db 519 MKLTDGSYFGEICLLTKG---RRTASVRADTYCRLYSLSVDNFEVLEVEYPMWRRAFEIV 575

Qy 637 -----ILMKK-----ARVLLKQKAK----- 651
Db 576 AIDRLDRIGKNSILLQKFOKDLNLTGTVFNQNEILLQIVKHDREVMVQAIPINYPQMTA 635

Qy 652 ---TAEATPPRKDL-----ALLFP-----P 668
Db 636 LNCISSTTTPSRMRQSPVYVATSLSHNLHSPSPSTQTPPSAILSPCSVTTAVCS 695

Qy 669 KEETPKLFTLLGGTGKASLARLLKLKREQAAQ---KKNESGEGEBEGKENEDKOKENED 725
Db 696 PIQSPLATRTFFHVASPTASQLSLMQPQQQLPOSQVQQTQTQTQQQQQQQQQQQQQQQ 755

Qy 726 KQENEDKGENEDKQGRPEPEKPLDRPCTASPTAVEEHSVVRTVLPGRGTSRQSL- 784
Db 756 QQQQQQQQQQQQQQQQQQQQQPPQFSGSTPKNEVHKSTQALHNTLTKVRLPLSASQPSLP 815

Qy 785 -----IISMAPSAEGGEEVLT 801
Db 816 HEVSTLIS-RPHPTVGESIASI 836

; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10771
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10771

Query Match          9.7%; Score 412.5; DB 4; Length 1109;
Best Local Similarity 23.9%; Pred. No. 2.1e-27;
Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

Qy 62 SEEPHTNIQDKLSKKN--SSGDLTTNPD---PQNAAEPTGTVPQKEMDPGKE-----Gp 111
Db 21 SSSSHGLHDSAEERLLTAEGDASPGEDRTFPLGAEP-----RPGSAAQPAASP 71

Qy 112 NSPQKPPAAPVINEYADAQLNLVKRMQRFTAL-YKKKLVEGDISSPEASQTAKTAV 170
Db 72 PPPQQPPQPASASCQPSVD-----TAIKVEGGAAGDQILPEAEVRLGOAGPM 120

Qy 171 PPVKESDDKPTHEHYELLWFKVKMPLTEYLKRIKLPN--SIDSYTD-RLYLLWLLVTL 227
Db 121 QRFQAMLPQGVNKFSLRMFGSQKAREQ-ERVKASGFWIIHPYSDFRY--WDLTMLL 177

Qy 228 AYNNWCWPIFLRVFPYOTADNIHNLWLIADIIICDIYLYDMLFIQPRLOQVRG-----G 281
Db 178 LMVGNLIIIPVGITF--FKDENTTPWIVNVVSDFFLIDLIV-----LNFRTGIVVEDNT 230

Qy 282 DIIVDSNELKHYRTSTKFDLDVASIIPFDICYL-----FFGFNPMF 323
Db 231 EILDPQRIKMKYLSW-FMVDFISSIPVDVIFILVETRIDSEVYKTARALRIVRFTKIL 289

Qy 324 RANRMLKYTSPFEFNHLESIMDKAY-----IYRVIRITGVLLFTLHINACVYVWASNYE 378
Db 290 SLRLRLSLRILYTHQWEEIFHMTYDLASAVVRIVNLIIGMMLLCHWDGCLQFLVPMLO 349

Qy 379 GIGTTRW-----VYDGEENLYRCYYWAVRTLITIG-GLPEPQTLFEIVFOLLNFFSGV 431
Db 350 DFDPDCWVSINNWNVNSWKGQSYALFKAMSHMLCIGYRQAPVGMSDVWLTMLSMIVGA 409

Qy 432 FVFSLLIGOMRDVIGAATANQNYFRACDDTIAYNNYSIPKLQKRVRTWYETWDSQR 491
Db 410 TCYAMFIHATALIQSLDSSRRQYQEKYQVEQYMSFHKLPDPDTRQRIHDYEHRYQOG-K 468

Qy 492 MLDSDLLKTLPTTVQLALADIVNPS---IISKVDLPKGCOTQMTYDMLRLKSLVLYLPG 548
Db 469 MFEESILGELSEPLUREE---INFNCRKLVASMLPFANADPNFTVSMTLKRLFEVFPQG 525

Qy 549 DFVCKKGBIGKEMYIIKHGEVQVL-GSPDGTKVLYTLKAGSVFGEISILAAAGGNRRRTAN 607
Db 526 DVIIRREGTIGKKWYFIQHGVSVLTKGNKETK---LADGSYFGEICLLTRG---RRTAS 578

Qy 608 VVAHGFANLLTLDKKTLLQEIIVHYPDSEIRILMKKA 642
Db 579 VRADTYCRLYSLSVDNFEVLEVEYF-----MWRRA 608
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RESULT 15
US-09-949-016-6036
; Sequence 6036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6036
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6036

Query Match 9.6%; Score 405.5; DB 4; Length 889;
Best Local Similarity 23.0%; Pred. No. 6.4e-27;
Matches 170; Conservative 116; Mismatches 301; Indels 151; Gaps 29;

Qy 83 TTNPDPQNAABPTGTVPQK-----EMDPKGEKSPQNKPPAAPVINEYADLAQLHLV 136
Db 19 TTGPPPPPPPP-----PKQPPPPPPPPPPGPGPAPQHPHRAEALPPEADE--GGPR 72

Qy 137 KMRQRTALYKKLVGLDLSPEASQ-----TAKPTAVP----- 171
Db 73 GLRSRDSGCCPGTGPCAATAGKSPNGECGRGECGPGAGPGAPGPKVFSFCRGAAS 132

Qy 172 -----PVKESDD-----KPTHEYRLWFKVKKMPLE 199
Db 133 GPAPGPGPAEAGSEAGPAGEPRGSQASFMQRFGALLQGVNKFSLRMFGSKAVERE 192

Qy 200 YLKRKLPNLS--IDSYTD--RLYLLWLLVTLAYNWCWFIPLRVF--PYQTADNIHWL 254
Db 193 Q-ERVKSAGAWIHPYSDFRY--WDFTLFLFMVGNLIIIPVGITFFKDETTAP----WI 245

Qy 255 IADIICDIYLMFTQPLQFVRG-----GDIIVDSNELKHYRTSTKFDLVASII 308
Db 246 VFNVSVDTFFLMDLV-----LNFRTGIVIEDNTBIILDPEKIKKY-LRTWVVDVFSI 299

Qy 309 PFDICYL-----PFGFNPMFRANMLKYTSFFFNHLESIMDKAY- 349
Db 300 PVDYIFLIVEGIDSEVVKTAARURIVRFTKILSLRLRLSLRIRYIHOWEEIFHMTYD 359

Qy 350 ----IYRVIRTTGYLLFIHINACVYVWASNYEGIGTTRWV-YDGEKNE-----YLRCY 399
Db 360 LASAVMRICNLISMLLLCHWDGCLQFLVPMLODPFPCWVSINGMWNHWSSELYSPALP 419

Qy 400 WAVTLTITIG-GLPEPOTLFEIVFQNLNPFSGVVFSSLIQOMRDVIGAAATANQNYFRAC 458
Db 420 KAMSHMLCIGYGRQAPESMTDILWTLMSIVGATCYAMFIGHATALIQLDSSRRQYQEK 479

Qy 459 MDDTIAWMNYSIPKLQKRVRTWYETWDSQRMDESLLKTLPTTVQLALADNFS- 517
Db 480 YKQVEQYMSFHLKPADFRQKIDHYEHRYQG-KMFDEDSILGELNGPLREEI---VNFNC 535

Qy 518 --IISKVDLPKGCOTMIYDMLLRLKSVLYLPDGFVCKKGIGKEMVIIKHGEVOVLGGP 575
Db 536 RKLVASNPFLFANADPNFVTAMLTKLKFEVQPGDYIIRREGTIGKKNYFIQHGVSVL--T 593

Qy 576 DGTKVLVTLKAGSVFGISLAAAGGNRRRTANVVAHGAFANLLTLDKTLQBIILVHYDSE 635

Db 594 KGNKEM-KLSDGSYFGEICLLTRG---RRTASVRAADTYCRLYSLSVONFNVELEYPMMR 649
Qy 636 RILMKARVLLKQAKTAEATPPRKDLALLFPKPKEETPKLFTLLGGTGKASLARLLKLK 695
Db 650 RAFETVAIDRLDRIGK-----KNSILLHKVQHD---LNSGVFNQENAIQIIVKYD 698
Qy 696 REQAQKKENSEGGELEG 713
Db 699 REMVQQ-----AELQVRVG 712

Search completed: March 27, 2005, 21:00:18
Job time : 58 secs

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OM protein - protein search, using sw model

Run on: March 27, 2005, 18:01:32 ; Search time 129 Seconds
(without alignments)
2425.497 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFSLTKVKNVKPIGENNEN.....PSAEGGSEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	5	AAE15982 Human cyc
2	4231	99.9	809	5	AAE15983 Human CNG
3	4231	99.9	809	5	AAE15985 Human CNG
4	4229	99.9	809	5	AAE15984 Human CNG
5	4228	99.9	809	5	AAE15986 Human CNG
6	1948.5	46.0	1250	8	ABM83979 Human dia
7	1781.5	42.1	652	4	ABG27471 Novel hum
8	1103	26.1	1037	4	ABG66545 Drosophil
9	1088	25.7	644	4	ABG05466 Novel hum
10	955	22.6	747	4	ABG11969 Novel hum
11	906	21.4	237	6	ABR33396 Amino aci
12	902	21.3	237	6	ABP98584 Amino aci
13	850	20.1	694	5	AAE15987 Human CNG
14	850	20.1	694	7	AAE38591 Human CNG
15	831.5	19.6	683	7	ADD48638 Rat Prote
16	829	19.6	663	5	AAE15982 Cow HBMYC
17	829	19.6	663	6	ABG74912 Bovine CN
18	826.5	19.5	698	8	ADQ67650 Novel hum
19	825.5	19.5	664	5	AAE15987 Variant H
20	824	19.5	663	6	ABG74914 Bovine CN
21	823	19.4	663	6	ABG74913 Bovine CN
22	821.5	19.4	664	6	ABG72530 Novel hum
23	820.5	19.4	664	5	AAE15987 HBMYCNG
24	820	19.4	732	5	AAE15987 Rabbit HB
25	819.5	19.4	664	4	AAE04894 Human tra

26	819.5	19.4	664	5	ABB78066 Amino aci
27	819.5	19.4	664	6	ABG72529 Novel hum
28	819.5	19.4	664	6	ABU12049 Human NOV
29	819.5	19.4	664	6	ABP98475 Amino aci
30	818.5	19.3	690	7	ADD93244 Cyclic nu
31	818.5	19.3	690	8	ADI38341 Human pro
32	817	19.3	686	7	ADD48640 Human pro
33	816.5	19.3	664	8	ADR09903 Human pro
34	815	19.2	690	5	AAE15988 Human CNG
35	804	19.0	664	5	AAE15988 Rat HBMYC
36	804	19.0	664	6	AAE37219 Rat CNG c
37	804	19.0	664	7	ADF56504 Rat CNG c
38	802	18.9	664	7	ADF56501 Modified
39	795	18.8	664	6	AAE37220 Rat CNG c
40	791	18.7	664	7	ADF56502 Modified
41	791	18.7	664	6	AAE37224 Rat CNG c
42	790	18.7	664	6	AAE37223 Rat CNG c
43	790	18.7	664	6	AAE37222 Rat CNG c
44	782	18.5	664	6	AAE37222 Rat CNG c
45	777.5	18.4	664	5	AAE15982 Mouse HBM

ALIGNMENTS

RESULT 1
AAE15982
ID AAE15982 standard; protein; 809 AA.
AC AAE15982;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cyclic nucleotide-gated cation channel 3 beta subunit protein.
XX
KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
KW male infertility; genetic defect; reporter-ligand interaction; CNG;
KW viral infection; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 210..661
FT /note= "Conserved region; this region also function as an epitope and is referred in claim 1"
XX
FN WO200188090-A2.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-US015814.
XX
XX 15-MAY-2000; 2000US-0204445P.
XX
XX 14-MAY-2001; 2001US-00855828.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Creech CD, Jegla TJ;
XX
XX WPI; 2002-089847/12.
XX
XX N-PSDE; AAD25729.
XX
XX New polypeptide, useful for screening for modulators of cyclic nucleotide-gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.
XX
XX Claim 12; Fig 4; 83pp; English.
XX
XX The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha

CC	subunits that are expressed in retina. CNG3B polypeptides are useful for	
CC	screening modulators of CNGs which are useful as contraceptives and for	
CC	treating various disorders involving cation channels, e.g. vision	
CC	disorders and male infertility. Polynucleotides of the invention are	
CC	useful for transfection of cells in vitro and in vivo, to correct	
CC	acquired and inherited genetic defects, cancer and viral infections.	
CC	Sequences of the invention are useful as reporter molecules in assays and	
CC	detection systems, to measure changes in cation concentration, membrane	
CC	potential, current flow, ion flux, transcription, signal transduction,	
CC	reporter-ligand interactions and second messenger concentrations, in	
CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs	
CC	in a computer system and for examining expression and regulation of	
CC	cation channels. The present sequence is human CNG3B protein	
XX		
SQ	Sequence 809 AA;	
	Query Match 100.0%; Score 4234; DB 5; Length 809;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MFKSLTKVNVKVPVIGENNENEGSSRNREGSHPSNOSQQTAAQENKGEKSLTKSTPV 60	
DB	1 MFKSLTKVNVKVPVIGENNENEGSSRNREGSHPSNOSQQTAAQENKGEKSLTKSTPV 60	
QY	61 TSEEPHTNIQDKLSKKNSSGDLTTNPDQNAAEPTGTVPQKEMDPGKGGPNSPQNKPPA 120	
DB	61 TSEEPHTNIQDKLSKKNSSGDLTTNPDQNAAEPTGTVPQKEMDPGKGGPNSPQNKPPA 120	
QY	121 APVINEYADAQHLNLRVQRQRTALYKVKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180	
DB	121 APVINEYADAQHLNLRVQRQRTALYKVKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180	
QY	181 TEHYVLLMFKVKKMPLETKRIKIPNSIDSVYDRLYLWLLVLTAYNNWCWFPLRL 240	
DB	181 TEHYVLLMFKVKKMPLETKRIKIPNSIDSVYDRLYLWLLVLTAYNNWCWFPLRL 240	
QY	241 VFPYQADNHWYLIADICIIYLYDMLFIQRLQFVRGGDIIVDSNELRKHRTSTKF 300	
DB	241 VFPYQADNHWYLIADICIIYLYDMLFIQRLQFVRGGDIIVDSNELRKHRTSTKF 300	
QY	301 QLDVASIIPFDICYLFPGFNPMFRANRMLKYTSFFFNHLESIMDKAYIYRVIRTTGYL 360	
DB	301 QLDVASIIPFDICYLFPGFNPMFRANRMLKYTSFFFNHLESIMDKAYIYRVIRTTGYL 360	
QY	361 LFTLHNACVYVWASNYEGITRWYDGEENYLRICYWAVRTLITIGGLPEPQTLFEI 420	
DB	361 LFTLHNACVYVWASNYEGITRWYDGEENYLRICYWAVRTLITIGGLPEPQTLFEI 420	
QY	421 VFOLLNPFSGVFVFSIIGQMRDVI GAATANQNYFRACMDTTIAYWNNYSIPKLVQKRV 480	
DB	421 VFOLLNPFSGVFVFSIIGQMRDVI GAATANQNYFRACMDTTIAYWNNYSIPKLVQKRV 480	
QY	481 TWYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSSIISKVDLPFGCDTQMIDMLRL 540	
DB	481 TWYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSSIISKVDLPFGCDTQMIDMLRL 540	
QY	541 KSVLYLPGDPVCKKGKIGKEMYIIKHGEVQVLGGPGTKVLTAKSGVGEISLLAAG 600	
DB	541 KSVLYLPGDPVCKKGKIGKEMYIIKHGEVQVLGGPGTKVLTAKSGVGEISLLAAG 600	
QY	601 GNRRTANVAHGFANLITLDKKTLOEILVHYDPSERILMKKARVLLKQAKTAETPPRK 660	
DB	601 GNRRTANVAHGFANLITLDKKTLOEILVHYDPSERILMKKARVLLKQAKTAETPPRK 660	
QY	661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKREQAQKKNSEGGEGEKENEDKQ 720	
DB	661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKREQAQKKNSEGGEGEKENEDKQ 720	
QY	721 KENEDKQKKNEDKQKKNEDKQKREPEKPLDREPTASTPIAVEEPHSHVRRVTLPRGTS 780	
DB	721 KENEDKQKKNEDKQKKNEDKQKREPEKPLDREPTASTPIAVEEPHSHVRRVTLPRGTS 780	
QY	781 RQSLIISMAPSAGGEEVLTIEVKEKAKQ 809	

DB	781 RQSLIISMAPSAGGEEVLTIEVKEKAKQ 809	
RESULT 2		
AAE15983		
ID	AAE15983 standard; protein; 809 AA.	
XX	AAE15983;	
AC	AAE15983;	
DT	26-MAR-2002 (first entry)	
XX		
DE	Human CNG3B protein variant #1 (R142K).	
XX		
KW	Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;	
KW	cyclic nucleotide-gated ion channel; contraceptive; vision disorder;	
KW	male infertility; genetic defect; reporter-ligand interaction; CNG;	
XX	viral infection; cancer; mutant; mutein; variant.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 142	
FT	/note= "Wild type Arg substituted with Lys"	
XX		
PN	WO200188090-A2.	
XX		
PD	22-NOV-2001.	
XX		
PF	15-MAY-2001; 2001WO-US015814.	
XX		
PR	15-MAY-2000; 2000US-0204445P.	
PR	14-MAY-2001; 2001US-00855828.	
XX		
PA	(ICAG-) ICAGEN INC.	
PI	Cresch CD, Jegla TJ;	
XX		
DR	WPI; 2002-089847/12.	
XX		
PT	New polypeptide, useful for screening for modulators of cyclic nucleotide	
PT	-gated ion channels, comprises the isolated cyclic nucleotide-gated	
PT	cation channel 3 beta subunit.	
XX		
PS	Disclosure; Page; 83pp; English.	
XX		
CC	The invention relates to human cyclic nucleotide-gated cation channel 3	
CC	beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member	
CC	of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms	
CC	functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha	
CC	subunits that are expressed in retina. CNG3B polypeptides are useful for	
CC	screening modulators of CNGs which are useful as contraceptives and for	
CC	treating various disorders involving cation channels, e.g. vision	
CC	disorders and male infertility. Polynucleotides of the invention are	
CC	useful for transfection of cells in vitro and in vivo, to correct	
CC	acquired and inherited genetic defects, cancer and viral infections.	
CC	Sequences of the invention are useful as reporter molecules in assays and	
CC	detection systems, to measure changes in cation concentration, membrane	
CC	potential, current flow, ion flux, transcription, signal transduction,	
CC	reporter-ligand interactions and second messenger concentrations, in	
CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs	
CC	in a computer system and for examining expression and regulation of	
CC	cation channels. The present sequence is human CNG3B protein variant	
CC	(R142K). Note: This sequence is not shown in the specification, but is	
CC	derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig	
CC	4 of the specification (AAE15982)	
XX		
SQ	Sequence 809 AA;	
	Query Match 99.9%; Score 4231; DB 5; Length 809;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 808; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	

Qy 1 MFSLTKVNVKVPKPIGENNENEGSSRRNEEGSHPSNQSQTTAQENKGEESLTKTSTPV 60
Db 1 MFSLTKVNVKVPKPIGENNENEGSSRRNEEGSHPSNQSQTTAQENKGEESLTKTSTPV 60
Qy 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGPNSPQNKPPA 120
Db 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGPNSPQNKPPA 120
Qy 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180
Db 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180
Qy 181 TEHYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWNCFIPLRL 240
Db 181 TEHYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWNCFIPLRL 240
Qy 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFTQPLRFQVRGGDIIVDSNELRKHRTSTKF 300
Db 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFTQPLRFQVRGGDIIVDSNELRKHRTSTKF 300
Qy 301 QLDVASIIPFDICVLFQFNPMFRANRMLKVTSPFNFHLESIMDKAYIYRVIRTTGYL 360
Db 301 QLDVASIIPFDICVLFQFNPMFRANRMLKVTSPFNFHLESIMDKAYIYRVIRTTGYL 360
Qy 361 LFIHINACVYVYASNYEGIGTRWYDGEYRCLYCYWAVRTLITIGGLPEPQTLFEI 420
Db 361 LFIHINACVYVYASNYEGIGTRWYDGEYRCLYCYWAVRTLITIGGLPEPQTLFEI 420
Qy 421 VFQLLNPFSGVVFSSLLIGQMRDVIGATATQNTYFRACMDDTIAYMNNYSIPKLQKVR 480
Db 421 VFQLLNPFSGVVFSSLLIGQMRDVIGATATQNTYFRACMDDTIAYMNNYSIPKLQKVR 480
Qy 481 TWYETWDSQRMLESDDLKLTPTVOLALAI DVNFSIISKVDLPFGCDTQMIYDMLRL 540
Db 481 TWYETWDSQRMLESDDLKLTPTVOLALAI DVNFSIISKVDLPFGCDTQMIYDMLRL 540
Qy 541 KSVLYLPGDFCKGKEIGKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Db 541 KSVLYLPGDFCKGKEIGKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Qy 601 GNRRTANVAVGFANLLDKTQELIYVHPDSEIRILMKARVLLKQAKTAETPPRK 660
Db 601 GNRRTANVAVGFANLLDKTQELIYVHPDSEIRILMKARVLLKQAKTAETPPRK 660
Qy 661 DLALLFPPEETPKLFTLLGSGTASLARIKLLKREQAOKKENSEGEGEKENEDKQ 720
Db 661 DLALLFPPEETPKLFTLLGSGTASLARIKLLKREQAOKKENSEGEGEKENEDKQ 720
Qy 721 KENEDKQKENEKEDKDKGREPEKPLDRPECTASPIAVBEEPHSVRRTVLPRTS 780
Db 721 KENEDKQKENEKEDKDKGREPEKPLDRPECTASPIAVBEEPHSVRRTVLPRTS 780
Qy 781 RQSLIISMAPSAEGEEVLTIEVKEKAKQ 809
Db 781 RQSLIISMAPSAEGEEVLTIEVKEKAKQ 809

RESULT 3

AAE15985
ID AAE15985 standard; protein; 809 AA.
XX AC AAE15985;
XX XX
DT 26-MAR-2002 (first entry)
XX DE Human CNG3B protein variant #3 (L675V).
XX KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
KW male infertility; genetic defect; reporter-ligand interaction; CNG;
KW viral infection; cancer; mutant; mutein; variant.
XX

OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 675 /note= "Wild type Leu substituted with Val"
XX WO20018090-A2.
XX 22-NOV-2001.
XX 15-MAY-2001; 2001WO-US015814.
XX 15-MAY-2000; 2000US-0204445P.
XX 14-MAY-2001; 2001US-00855828.
XX (ICAG-) ICAGEN INC.
XX Creech CD, Jegla TJ;
XX WPI; 2002-089847/12.
XX New polypeptide, useful for screening for modulators of cyclic nucleotide
gated ion channels, comprises the isolated cyclic nucleotide-gated
cation channel 3 beta subunit.
XX Disclosure; Page; 83pp; English.
XX The invention relates to human cyclic nucleotide-gated cation channel 3
beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
subunits that are expressed in retina. CNG3B polypeptides are useful for
screening modulators of CNGs which are useful as contraceptives and for
treating various disorders involving cation channels, e.g. vision
disorders and male infertility. Polynucleotides of the invention are
useful for transfection of cells in vitro and in vivo, to correct
sequences of inherited genetic defects, cancer and viral infections.
Sequences of the invention are useful as reporter molecules in assays and
detection systems, to measure changes in cation concentration, membrane
potential, current flow, ion flux, transcription, signal transduction,
reporter-ligand interactions and second messenger concentrations, in
vitro, in vivo and ex vivo. They are useful to construct models of CNGs
in a computer system and for examining expression and regulation of
cation channels. The present sequence is human CNG3B protein variant
(L675V). Note: This sequence is not shown in the specification, but is
derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
4 of the specification (AAE15982)
SQ Sequence 809 AA;
Query Match 99.9%; Score 4231; DB 5; Length 809;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 808; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFSLTKVNVKVPKPIGENNENEGSSRRNEEGSHPSNQSQTTAQENKGEESLTKTSTPV 60
Db 1 MFSLTKVNVKVPKPIGENNENEGSSRRNEEGSHPSNQSQTTAQENKGEESLTKTSTPV 60
Qy 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGPNSPQNKPPA 120
Db 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGPNSPQNKPPA 120
Qy 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180
Db 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPVKESDDKP 180
Qy 181 TEHYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWNCFIPLRL 240
Db 181 TEHYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWNCFIPLRL 240
Qy 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFTQPLRFQVRGGDIIVDSNELRKHRTSTKF 300
XX

Db 541 KSVLYLPGDFVCKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Qy 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVYPDSERILMKARVLLKQAKTAEATPPRK 660
Db 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVYPDSERILMKARVLLKQAKTAEATPPRK 660
Qy 661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720
Db 661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720
Qy 721 KENEDKQKENEKDKGKREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780
Db 721 KENEDKQKENEKDKGKREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780
Qy 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
Db 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809

RESULT 5

AAE15986
ID AAE15986 standard; protein; 809 AA.
AC AAE15986;

XX 26-MAR-2002 (first entry)
XX Human CNG3B protein variant #4 (G682S).

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
KW male infertility; genetic defect; reporter-ligand interaction; CNG;
KW viral infection; cancer; mutant; mutein; variant.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 682
FT /note= "Wild type Gly substituted with Ser"

XX WO200188090-A2.
XX 22-NOV-2001.
XX 15-MAY-2001; 2001WO-US015814.
XX 15-MAY-2000; 2000US-020445P.
XX 14-MAY-2001; 2001US-00855828.
XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;
XX WPI; 2002-089847/12.

XX New polypeptide, useful for screening for modulators of cyclic nucleotide
PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
FT cation channel 3 beta subunit.

XX Disclosure; Page; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3
CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
CC subunits that are expressed in retina. CNG3B polypeptides are useful for
CC screening modulators of CNGs which are useful as contraceptives and for
CC treating various disorders involving cation channels, e.g. vision
CC disorders and male infertility. Polynucleotides of the invention are
CC useful for transfection of cells in vitro and in vivo, to correct
CC acquired and inherited genetic defects, cancer and viral infections.

CC Sequences of the invention are useful as reporter molecules in assays and
CC detection systems, to measure changes in cation concentration, membrane
CC potential, current flow, ion flux, transcription, signal transduction,
CC reporter-ligand interactions and second messenger concentrations, in
CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
CC in a computer system and for examining expression and regulation of
CC cation channels. The present sequence is human CNG3B protein variant
CC (G682S). Note: This sequence is not shown in the specification, but is
CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
CC 4 of the specification (AAE15982)

XX Sequence 809 AA;

Query Match 99.9%; Score 4228; DB 5; Length 809;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKSLTKVNVKPIGNNENQSSRRNEEGSHPNQSOQTAAQENKGEKSLTKTSTPV 60
Db 1 MFKSLTKVNVKPIGNNENQSSRRNEEGSHPNQSOQTAAQENKGEKSLTKTSTPV 60
Qy 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPPQNAAEPTGTVEOKEMDPGKGPNSPONKPPA 120
Db 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPPQNAAEPTGTVEOKEMDPGKGPNSPONKPPA 120
Qy 121 APVINEYADAQLHNLVKRMQRQTALYKKLVGEGDLSSPEASPTAKPTAVPPVKESDDKP 180
Db 121 APVINEYADAQLHNLVKRMQRQTALYKKLVGEGDLSSPEASPTAKPTAVPPVKESDDKP 180
Qy 181 TEHYRLLWFKVKOMPLTEYLKRIKLNSIDSYTDRLYLLMLLVTLAYNWCNFIPLRL 240
Db 181 TEHYRLLWFKVKOMPLTEYLKRIKLNSIDSYTDRLYLLMLLVTLAYNWCNFIPLRL 240
Qy 241 VFYQTDADNTHYMLIADIICDIIYLYDMLFQPLRQFVRGGDIIVDSNELRKHRTSTKF 300
Db 241 VFYQTDADNTHYMLIADIICDIIYLYDMLFQPLRQFVRGGDIIVDSNELRKHRTSTKF 300
Qy 301 QLDVASIIPEDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYL 360
Db 301 QLDVASIIPEDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYL 360
Qy 361 LFIHINACVYVWASNYEGITTRWYDGEVQVQLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Db 361 LFIHINACVYVWASNYEGITTRWYDGEVQVQLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Qy 421 VFQLNFFSGVVFSSLIQMRDVIQATANQNTFRACMDDTIAYMNNYSIPKLQKRVK 480
Db 421 VFQLNFFSGVVFSSLIQMRDVIQATANQNTFRACMDDTIAYMNNYSIPKLQKRVK 480
Qy 481 TWYEYTWDSQRMLESLLKTLPTTVQLALADVNFISIISKVDLFGKCDTQMIYDMLLRL 540
Db 481 TWYEYTWDSQRMLESLLKTLPTTVQLALADVNFISIISKVDLFGKCDTQMIYDMLLRL 540
Qy 541 KSVLYLPGDFVCKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Db 541 KSVLYLPGDFVCKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600
Qy 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVYPDSERILMKARVLLKQAKTAEATPPRK 660
Db 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVYPDSERILMKARVLLKQAKTAEATPPRK 660
Qy 661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720
Db 661 DLALLFPKPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720
Qy 721 KENEDKQKENEKDKGKREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780
Db 721 KENEDKQKENEKDKGKREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780
Qy 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
Db 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809

DE Novel human diagnostic protein #11960.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS76156.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 42328; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques for restoring normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: the sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 747 AA;
XX
XX Query Match 22.6%; Score 955; DB 4; Length 747;
XX Best Local Similarity 32.8%; Pred. No. 5e-72;
XX Matches 231; Conservative 17; Mismatches 34; Indels 422; Gaps 6;
XX
XX 112 NSPQKPPAAVINEYADAQLHNLVKRMQRQTALYKKLVGDLSSPEASPTAKPTAVP 171
XX 44 NSPQKPPAAVINEYADAQLHNLVKRMQRQTALYKKLVGDLSSPEASPTAKPTAVP 103
XX
XX 172 PVKESDDKPTHEYRLVLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLLVLLVLTAVNW 231
XX 104 PVKESDDKPTHEYRLVLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLLVLLVLTAVNW 163
XX
XX 232 NCWFIPLRLVPPYQTADNIHLYLADIICDIYLYDMLFIQPRIQFVRGGDI 284
XX 164 NCCFIPLRLVPPYQTADNIHLYLADIICDIYLYDMLFIQPRIQFVRGGDIIRFQESYP 223
XX
XX 285 -----VD-----SNELRKHYRTSTKQL----- 302
XX 224 SFSPFWFVDCDDPNLTSYLERPEDTENNYYLRQLKCTWFMFEMLDQPLPMQNGKIEVTS 283
XX

QY 303 ----- 302
Db 284 EEEEEEMAGDIKYLNHCKMKKEELISGKLEDEGIEKENLATLEKIRKTQSGHLNVWVC 343
QY 303 ----- 302
Db 344 LSGSETTKPRNSGTGRRRKESKQLKAGSQREWLOVQIOTIGILMSEKAEMLTALYYTOHA 403
QY 303 -----DVASIIIP----- 310
Db 404 ARQFEGESKDIAASCIQYSWRVQDNEGLSLNREQERLLELEQKAELEWEEVVEHROTLE 463
QY 311 -----DICYLPFGFNPFRANRMLKYTSFFE----- 336
Db 464 TMQNDLTTISHAVFQNGELKEQLAKLQTGFMKLNENMEITSTPQSEHQHKKEPSEKLG 523
QY 337 -----FNH----- 339
Db 524 GLDSEEBALPLMPSIPEELESREAMVAFNLNSAVASABEEQAWPRGQLKEORGAMEKLQSH 583
QY 340 HLESIMDKAYIYR----- 352
Db 584 FMELMQEKVDLKEOMEKLERRCIOLSGSETDVIHHVTPELEVSADVAPEGIHQOPEGQ 643
QY 353 ----- 352
Db 644 GGDEGEAAGAAGAGAAGAGGIPPEGIVIIIGNDSSTHWPEDLPVGQDVDESDIDDP 703
QY 353 ---VIRTTGYLLFILHINACVYVWASNYEGITGTRVWYDGE 393
Db 704 DPVVIRTTGYLLFILHINACVYVWASNYEGITGTRVWYDGE 747

RESULT 11
ABR39396
ID ABR39396 standard; protein; 237 AA.
XX
AC ABR39396;
XX
XX 26-JUN-2003 (first entry)
XX
XX Amino acid sequence of human betalb.
XX
XX OCN1; OCN2; betalb; CNG; human;
XX olfactory cyclic nucleotide gated channel subunit.
XX
XX Homo sapiens.
XX
XX WO2003004611-A2.
XX
XX 16-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-US021184.
XX
XX 06-JUL-2001; 2001US-0303140P.
XX
XX 10-DEC-2001; 2001US-0337154P.
XX
XX (SENO-) SENOMYX INC.
XX
XX Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JE;
XX Servant G, Callamaras N;
XX
XX WPI; 2003-229406/22.
XX
XX N-PSDB; ABZ80565.
XX
XX Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b
XX olfactory cyclic nucleotide gated (CNG) channel subunits, useful for
XX identifying the CNG channel activators useful for enhancing smell.
XX
XX Disclosure; Page 86; 97pp; English.
XX
XX The present invention relates to a nucleotide sequences encoding human
XX CC

CC OCN1, OCN2, or betalb olfactory cyclic nucleotide gated (CNG) channel
CC subunit, its action being an olfactory CNG channel activity modulator. A
CC host cell which expresses human OCN1, OCN2 and/or betalb is useful in a
CC mammalian cell-based assay for the profiling and screening of putative
CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.
CC The method is used to identify a compound as one which particularly
CC modulates CNG activity based on a detectable change in fluorescence. The
CC test cell expresses each of the human OCN1, human OCN2 and human betalb
CC subunits. A fluorescence plate reader or a voltage imaging plate are used
CC to monitor changes in fluorescence. The compounds that activate olfactory
CC CNG channel enhance smell and can be used to make foods more palatable
CC for individuals with attenuated olfactory function. The present sequence
CC represents the amino acid sequence of human betalb
XX
SQ Sequence 237 AA;

Query Match 21.4%; Score 906; DB 6; Length 237;
Best Local Similarity 72.8%; Pred. No. 1.4e-68;
Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;
QY 417 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATATQNYFRACMDDTIAYMNNYSIPKLQV 476
DB 1 LFEIVFOLLNFTGTGFAFSVMIGQMRDVVGATAGTYYRSCMDSTVKYNNFYKIPKSVQ 60
QY 477 KRVRTWYEYTWDSORMLDESLLKTLPTTVQALALADVNFSIISKVDLFGCDTQMIYDM 536
DB 61 NRKVTWYEYTWHSQGLDESELMVQLPDKMRDLDAIDVNNYVSKVALFQGCDDQMFDM 120
QY 537 LLRLKSVLYLPDGFVCKKGEIGKEMYYIKHGEVQVVGPDGPKVLTGKAGSVFGEISLL 596
DB 121 LKRLSVVYLPNDYVCKKGEIGREMYIIQAGQVQVVGPDGPKSVLTLKAGSVFGEISLL 180
QY 597 AAGGNNRTANVVAHGFANLLTLDKTLOETLVHYPDSERILMKKARVLLKQKAK 651
DB 181 AVGGNNRTANVVAHGFANLLTLDKTLOETLVHYPDSERILMKKARVLLKQKAK 651

RESULT 12
ABP98584
ID ABP98584 standard; protein; 237 AA.
XX AC ABP98584;
XX AC
DT 26-JUN-2003 (first entry)
XX
XX Amino acid sequence of rat betalb.
XX
XX OCN1; OCN2; betalb; CNG; rat;
XX Olfactory cyclic nucleotide gated channel subunit.
XX
XX Rattus sp.
XX
XX WO2003004611-A2.
XX
XX 16-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-US021184.
XX
XX 06-JUL-2001; 2001US-0303140P.
XX
XX 10-DEC-2001; 2001US-0337154P.
XX
XX (SENO-) SENOMYX INC.
XX
XX Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JE;
XX Servant G, Callamaras N;
XX WPI; 2003-229406/22.
XX
XX Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b
XX olfactory cyclic nucleotide gated (CNG) channel subunits, useful for
XX identifying the CNG channel activators useful for enhancing smell.
XX
XX Disclosure; Page 86; 97pp; English.

XX The present invention relates to a nucleotide sequences encoding human
CC OCN1, OCN2, or betalb olfactory cyclic nucleotide gated (CNG) channel
CC subunit, its action being an olfactory CNG channel activity modulator. A
CC host cell which expresses human OCN1, OCN2 and/or betalb is useful in a
CC mammalian cell-based assay for the profiling and screening of putative
CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.
CC The method is used to identify a compound as one which particularly
CC modulates CNG activity based on a detectable change in fluorescence. The
CC test cell expresses each of the human OCN1, human OCN2 and human betalb
CC subunits. A fluorescence plate reader or a voltage imaging plate are used
CC to monitor changes in fluorescence. The compounds that activate olfactory
CC CNG channel enhance smell and can be used to make foods more palatable
CC for individuals with attenuated olfactory function. The present sequence
CC represents the amino acid sequence of rat betalb
XX
SQ Sequence 237 AA;

Query Match 21.3%; Score 902; DB 6; Length 237;
Best Local Similarity 72.3%; Pred. No. 3e-68;
Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;
QY 417 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATATQNYFRACMDDTIAYMNNYSIPKLQV 476
DB 1 LFEIVFOLLNFTGTGFAFSVMIGQMRDVVGATAGTYYRSCMDSTVKYNNFYKIPKSVQ 60
QY 477 KRVRTWYEYTWDSORMLDESLLKTLPTTVQALALADVNFSIISKVDLFGCDTQMIYDM 536
DB 61 NRKVTWYEYTWHSQGLDESELMVQLPDKMRDLDAIDVNNYVSKVALFQGCDDQMFDM 120
QY 537 LLRLKSVLYLPDGFVCKKGEIGKEMYYIKHGEVQVVGPDGPKVLTGKAGSVFGEISLL 596
DB 121 LXELRSVYLPNDYVCKKGEIGREMYIIQAGQVQVVGPDGPKSVLTLKAGSVFGEISLL 180
QY 597 AAGGNNRTANVVAHGFANLLTLDKTLOETLVHYPDSERILMKKARVLLKQKAK 651
DB 181 AVGGNNRTANVVAHGFANLLTLDKTLOETLVHYPDSERILMKKARVLLKQKAK 651

RESULT 13
AAE15987
ID AAE15987 standard; protein; 694 AA.
XX AC AAE15987;
XX AC
DT 26-MAR-2002 (first entry)
XX
XX Human CNGA3 protein.
XX
XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
XX cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
XX male infertility; genetic defect; reporter-ligand interaction; CNG;
XX viral infection; cancer; CNGA3 protein.
XX
XX Homo sapiens.
XX
XX WO200188090-A2.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-US015814.
XX
XX 15-MAY-2000; 2000US-0204445P.
XX
XX 14-MAY-2001; 2001US-00855828.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Creech CD, Jegla TJ;
XX WPI; 2002-089847/12.
XX
XX New polypeptide, useful for screening for modulators of cyclic nucleotide
XX -gated ion channels, comprises the isolated cyclic nucleotide-gated

Query Match	20.1%;	Score 850;	DB 5;	Length 694;
Best Local Similarity	30.0%;	Pred. No. 4.2e-63;		
Matches	225;	Conservative 149;	Mismatches 269;	Indels 106;
Gaps	22;			
QY	27	NEEGSHPSNQSQQTTAAEENKGBEKSJTKSTPTVTSEEPHTNIQDKLSKKNSSGDLTNP	86	
DB	5	NTQISHPS-----RTHUKVK-----TSRDNLNRAENGSLRAHSSSEETS--	43	
QY	87	DPQVAAEPTGTVPQEKEMDPCKEGPNSPQNKPPAAPVINEYADAAQLHNLVKRMQRITALY	146	
DB	44	---SVLQP-GIAMETRGADSGGSGFTGQ-----GIARLSRLFLLRWAARH	87	
QY	147	KKKLVEGDLSSP-----EASPTAKTAPVPPVKESDDKPTHEYHYRLWLFVKKMWPL	197	
DB	88	VHHQDQGPDSFPDRFRGAELKEVSSQSNQAQNVGSEQEPADRG-----RSAW-----	136	
QY	198	-----TEYLKRILKLPNSI--DSYTDRLYLMLLVLTLAYNNWCWFFPLRLVFPYQT	246	
DB	137	AKCNTWTSNTEEEKTKKKDAIVDPSSNLRYRWLTATIALPVPYNNYLLICRACFDELQ	196	
QY	247	ADNIHWLIAADIICDIITYLDMLEFIQRLQFVRGGDIIVDSNEULRKHRTSTKFPOLDVAS	306	
DB	197	SEYLMMLWLVDYSADVLYVLDLV--VRARTGFEQGLMVSDTNRLWQHYKTTTQPKLDVLS	255	
QY	307	IIPFDICYLFFGN--PMFRANRLMKYTSFFEFNHLESIMDKAVIYRVIRTTGYLLFILH	365	
DB	256	LVPTDLAYLVKGTNYPEVRNRLKFSRLFEFFDRTETRTNYPNMFRIGNLVLYIIHH	315	
QY	366	INACVYVWASNYSGICTRWVYDG-----EGNEYLRCYVAVRTLIIIGGLPEPOTL	417	
DB	316	WNACIYPAISKFTGFGFDSWVYPNISIEPHGRLSRKVIYSLYNSTLTLTIGETPPPVKD	375	
QY	418	FEIVFOLLNFFSGVFPSSLIGOMRDVIGAATANQYFRACMDDTIAYMNNYSIPKLVOK	477	
DB	376	EEVLFVVVDVLGVLPATIVGNVGSIMSNWRASRAEFQAKISIKQYMFRTKDOLET	435	
QY	478	RVRTWYEYTWDSQRMLEDSELLKTLPTVQALAIADYNFSIIISKVDLFKGCDTQMIYDML	537	
DB	436	RVIRWFEDYLWANKTVDDEKEVLKSLPKDKAEIATINVHLDTLKKVRFQDCEAGLLVELV	495	
QY	538	LRKSLVLYLPDGFVCKKGETGKEMYIIKHGEVQVLGGPDGKTUVLTUKAGSVFGEISLLA	597	
DB	496	LKLRTVPFSPGDYICKKGDIKGEMYIINEGKLAV--ADDGVTQPVVLSDGYSFGEISILN	554	
QY	598	AGG--GNRRATANVAHGFRANLLTLDCKTLOETIIIVHYPPDSERTIIMKKAR--VLLKQK--	650	
DB	555	IKGSKSGNRRATANIRSIGYSDLPCLSKDDLMWEALTEYPEAKKALBEKGRIILMKNDNLIDE	614	
QY	651	KTAEATPPPKDXDLALLFPPEKETPKLFKTLJGGTGCKASLARLL-----KLKREQAQK	702	

Db	615	EIARAGADPDKL-----EKEVQLGSL--DTLQTRFARLLAEYNATQMKMKORLSQLE	666
Qy	703	KENSEGEE---EGKENEDKQKEDKQK	728
Db	667	SOVKGSGDKPLADGEVPCDATK--TEDKQK	694
RESULT 14			
AAE38591			
ID	AAE38591	standard; protein; 694 AA.	
AC	AAE38591;		
XX	04-DEC-2003	(first entry)	
XX	Human CNG channel alpha 3 potassium channel (KCNQ2).		
XX	Human; urological disorder; urinary incontinence; gene therapy; cancer;		
KW	kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;		
KW	urethra; overflow urinary incontinence; stress urinary incontinence;		
KW	nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;		
KW	CNG channel alpha 3 potassium channel; KCNQ2.		
OS	Homo sapiens.		
XX	WO2003061573-A2.		
XX	31-JUL-2003.		
XX	16-JAN-2003;	2003WO-US001450.	
XX	18-JAN-2002;	2002US-0349511P.	
PR	28-FEB-2002;	2002US-0360500P.	
PR	15-MAR-2002;	2002US-0365041P.	
PR	13-APR-2002;	2002US-0374063P.	
PR	14-AUG-2002;	2002US-0403468P.	
PR	27-SEP-2002;	2002US-0414262P.	
PR	21-OCT-2002;	2002US-0419986P.	
PR	05-NOV-2002;	2002US-0423809P.	
PR	26-NOV-2002;	2002US-0429797P.	
XX	(MILL-) MILLENNIUM PHARM INC.		
XX	Silos-Santiago I, Karicheti V;		
XX	WFI; 2003-598705/56.		
DR	N-PSDB; AAD58492.		
XX	Identifying a compound for treating urological disorders, for example		
PT	urinary incontinence by assaying the ability of the compound to modulate		
PT	the nucleic acid expression or polypeptide activity.		
XX	Disclosure; Page 159-160; 0pp; English.		
PS			
XX	The present relates to a method for identifying a compound for treating		
CC	urological disorders e.g. urinary incontinence including overactive/		
CC	oversensitive bladder, overflow urinary incontinence, stress urinary		
CC	incontinence caused by dysfunction of the bladder, urethra or central or		
CC	peripheral nervous system, prostatitis, benign prostatic hyperplasia,		
CC	cancer of the prostate or kidney disorders. The method is also useful for		
CC	modulating hyperplasia in a cell and treating a subject having a		
CC	urological disorder. The invention is also used in gene therapy. The		
CC	present sequence is human CNG channel alpha 3 potassium channel (KCNQ2)		
XX			
SQ	Sequence 694 AA;		
Query Match			
Best Local Similarity 30.0%; Score 850; DB 7; Length 694;			
Matches 225; Conservative 149; Mismatches 289; Indels 106; Gaps 22			
Qy	27	NEEGSHPSNOQTTAQENKGBEKSILKTSPTVTSEPTNIDQLSKNSSGDLTTNP	86

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 27, 2005, 20:58:17 ; Search time 1171 Seconds
(without alignments)
228.745 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSABGGSEVLTVIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	11	US-09-855-828-1
2	4228	99.9	809	11	US-09-855-828-1
3	906	21.4	237	15	US-10-189-507-11
4	902	21.3	237	15	US-10-189-507-7
5	850	20.1	694	10	US-09-842-758-75
6	850	20.1	694	11	US-09-855-828-14
7	850	20.1	694	14	US-10-345-680-26
8	850	20.1	694	15	US-10-174-333-75
9	829	19.6	663	14	US-10-029-677-16
10	825.5	19.5	664	14	US-10-029-677-24
11	820.5	19.4	664	14	US-10-029-677-2
12	820	19.4	732	10	US-09-842-758-73
13	820	19.4	732	14	US-10-029-677-15

14	820	19.4	732	15	US-10-174-333-73	Sequence 73, Appl
15	819.5	19.4	664	9	US-09-735-927-2	Sequence 2, Appl
16	819.5	19.4	664	13	US-10-034-843-2	Sequence 2, Appl
17	819.5	19.4	664	14	US-10-168-651-7	Sequence 7, Appl
18	819.5	19.4	664	14	US-10-114-153-18	Sequence 18, Appl
19	818.5	19.3	664	9	US-09-735-927-4	Sequence 4, Appl
20	817	19.3	690	11	US-09-855-828-15	Sequence 15, Appl
21	804	19.0	664	14	US-10-029-677-18	Sequence 18, Appl
22	804	19.0	664	14	US-10-087-217-2	Sequence 2, Appl
23	804	19.0	664	14	US-10-295-573-8	Sequence 8, Appl
24	802	18.9	664	14	US-10-295-573-5	Sequence 5, Appl
25	795	18.8	664	14	US-10-087-217-4	Sequence 4, Appl
26	791	18.7	664	14	US-10-087-217-6	Sequence 6, Appl
27	791	18.7	664	14	US-10-295-573-6	Sequence 6, Appl
28	782	18.5	664	14	US-10-087-217-8	Sequence 8, Appl
29	777.5	18.4	664	14	US-10-029-677-17	Sequence 17, Appl
30	773	18.3	634	14	US-10-295-573-7	Sequence 7, Appl
31	656	15.5	578	10	US-09-842-758-28	Sequence 28, Appl
32	656	15.5	578	15	US-10-174-333-28	Sequence 28, Appl
33	655	15.5	575	9	US-09-735-932-2	Sequence 2, Appl
34	655	15.5	575	9	US-09-927-267-1	Sequence 1, Appl
35	655	15.5	575	10	US-09-842-758-30	Sequence 30, Appl
36	655	15.5	575	14	US-10-207-951-2	Sequence 2, Appl
37	655	15.5	575	15	US-10-174-333-30	Sequence 30, Appl
38	653	15.4	575	16	US-10-311-624-1	Sequence 1, Appl
39	640	15.1	575	9	US-09-735-932-4	Sequence 4, Appl
40	640	15.1	575	9	US-09-927-267-16	Sequence 16, Appl
41	640	15.1	575	10	US-09-842-758-74	Sequence 74, Appl
42	640	15.1	575	15	US-10-174-333-74	Sequence 74, Appl
43	450.5	10.6	239	15	US-10-189-507-5	Sequence 5, Appl
44	449.5	10.6	239	15	US-10-189-507-9	Sequence 9, Appl
45	437	10.3	239	15	US-10-189-507-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-855-828-1
; Sequence 1, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creece, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human cyclic nucleotide-gated cation channel (CNG)
; OTHER INFORMATION: 3B (CNG3B)
; US-09-855-828-1

Query Match	100.0%;	Score 4234;	DB 11;	Length 809;
Best Local Similarity	100.0%;	Pred. No. 3.8e-301;		
Matches 809;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1	MFKSLTKVKNVKPIGENNENEQSSRRNEGSHPSNQSQTTAQENKGEKSLTKSTPV	60	
Db	1	MFKSLTKVKNVKPIGENNENEQSSRRNEGSHPSNQSQTTAQENKGEKSLTKSTPV	60	
Qy	61	TSEEPHTNIQDKLSKKNSGDLTTPDPQNAAEPTGTVPQKEMDPKSGNSQNKPPA	120	
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QY 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180
DB 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180
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DB 181 TEHYRLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240
QY 241 VFPYQTADNIHYWLIADIIICDIYLYDMLFIQPLRFVVRGGDIIVDSNELRKHRTSTKF 300
DB 241 VFPYQTADNIHYWLIADIIICDIYLYDMLFIQPLRFVVRGGDIIVDSNELRKHRTSTKF 300
QY 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360
DB 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360
QY 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQVGGDIIVDSNELRKHRTSTKF 420
DB 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQVGGDIIVDSNELRKHRTSTKF 420
QY 421 VQQLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480
DB 421 VQQLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480
QY 481 TWYETWDSQRMLESLLKTLPTTVQLALADIVNFSISKVDLFKGCDDTQMIYDMLLRL 540
DB 481 TWYETWDSQRMLESLLKTLPTTVQLALADIVNFSISKVDLFKGCDDTQMIYDMLLRL 540
QY 541 KSVLYLPDGFVCKGKEIGKEMYIIKHGEVQVGGDIIVDSNELRKHRTSTKF 600
DB 541 KSVLYLPDGFVCKGKEIGKEMYIIKHGEVQVGGDIIVDSNELRKHRTSTKF 600
QY 601 GNRRTANVVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK 660
DB 601 GNRRTANVVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK 660
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DB 661 DLALLFPKKEETPKLFKTLGGTGKASLARLLKREQAQKENSEGEGEENEDKQ 720
QY 721 KENEDKQKENEKEDKQKREPEEKPLDRPECTASPIAVEBEPHSVRTVLPRGTS 780
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QY 781 RQSLIISMAPSABGGEVLTIEVKEKAKQ 809
DB 781 RQSLIISMAPSABGGEVLTIEVKEKAKQ 809

RESULT 2

US-09-855-828-13
; Sequence 13, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Crech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855, 828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CNG3B
US-09-855-828-13

Query Match 99.9%; Score 4228; DB 11; Length 809;
Best Local Similarity 99.9%; Pred. No. 1.1e-300;
Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MFKSLTKVNVKXPIGNNENESRRNEEGSHPSNQSQQTTAQEENKGBEKSILKTSTPV 60
DB 1 MFKSLTKVNVKXPIGNNENESRRNEEGSHPSNQSQQTTAQEENKGBEKSILKTSTPV 60
QY 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPONAABPTGTVPEQKEMDPGKGGPNSPQNKPPA 120
DB 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPONAABPTGTVPEQKEMDPGKGGPNSPQNKPPA 120
QY 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180
DB 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180
QY 181 TEHYRLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240
DB 181 TEHYRLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240
QY 241 VFPYQTADNIHYWLIADIIICDIYLYDMLFIQPLRFVVRGGDIIVDSNELRKHRTSTKF 300
DB 241 VFPYQTADNIHYWLIADIIICDIYLYDMLFIQPLRFVVRGGDIIVDSNELRKHRTSTKF 300
QY 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360
DB 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360
QY 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQVGGDIIVDSNELRKHRTSTKF 420
DB 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQVGGDIIVDSNELRKHRTSTKF 420
QY 421 VQQLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480
DB 421 VQQLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480
QY 481 TWYETWDSQRMLESLLKTLPTTVQLALADIVNFSISKVDLFKGCDDTQMIYDMLLRL 540
DB 481 TWYETWDSQRMLESLLKTLPTTVQLALADIVNFSISKVDLFKGCDDTQMIYDMLLRL 540
QY 541 KSVLYLPDGFVCKGKEIGKEMYIIKHGEVQVGGDIIVDSNELRKHRTSTKF 600
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RESULT 3

US-10-189-507-11
; Sequence 11, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEX
; APPLICANT: ADLER, JON ELLIOT

APPLICANT: SERVANT, GUY
APPLICANT: CALLAMARAS, NICHOLAS
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
TITLE OF INVENTION: SMELL MODULATORS
FILE REFERENCE: 078003-0291567
CURRENT APPLICATION NUMBER: US/10/189,507
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/303,140
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/337,154
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
US-10-189-507-11

Query Match 21.4%; Score 906; DB 15; Length 237;
Best Local Similarity 72.8%; Pred. No. 3.9e-58;
Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

Qy 417 LFEIVFOLLNPFSGVFFSSLIQMRDVGIGAAATANQNYFRACMDDTIAYMNNYSIPKLQV 476
Db 1 LFEIVFOLLNFTGTFAPFVSMIGQMRDVVGAATAGQTYRSCMDSTVKYMFYKIPKSVQ 60

Qy 477 KRVTWYETWDSQRMDESLTKTLPTTVQLALAIQVNFIIISKVDLFGKCDTQMIYDM 536
Db 61 NRVTWYETWHSQGMDESELMVQLPKMRDLDAIDVNNIVSKVALFQCDRQMIYDM 120

Qy 537 LLRLKSVLYLPGDFVCKKGEGIKEMYIIKHGEVQVLGGPDGKTVLVTLKAGSVFGEISLL 596
Db 121 LKRLRSVYLPNDYVCKKGEGIKEMYIIQAQGVQVLGGPDGKSVLVTLKAGSVFGEISLL 180

Qy 597 AAGGNRRRTANVAHGFANLLTLDKKTLQELVHYPDSERILMKARVLLKQKAK 651
Db 181 AVGGNRRRTANVAHGFNTLFDLKKDLNEILVHYPESQKLLRKKARRMLRNNK 235

RESULT 4
US-10-189-507-7
Sequence 7, Application US/10189507
Publication No. US20030228633A1
GENERAL INFORMATION:
APPLICANT: ZOLLER, MARK
APPLICANT: XU, HONG
APPLICANT: STASZEWSKI, LENA
APPLICANT: MOYER, BRYAN
APPLICANT: PRONIN, ALEX
APPLICANT: ADLER, JON ELLIOT
APPLICANT: SERVANT, GUY
APPLICANT: CALLAMARAS, NICHOLAS
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
TITLE OF INVENTION: SMELL MODULATORS
FILE REFERENCE: 078003-0291567
CURRENT APPLICATION NUMBER: US/10/189,507
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/303,140
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/337,154
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 237
TYPE: PRT
ORGANISM: Rattus sp.
US-10-189-507-7

Query Match 21.3%; Score 902; DB 15; Length 237;
Best Local Similarity 72.3%; Pred. No. 7.7e-58;
Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

Qy 417 LFEIVFOLLNPFSGVFFSSLIQMRDVGIGAAATANQNYFRACMDDTIAYMNNYSIPKLQV 476
Db 1 LFEIVFOLLNFTGTFAPFVSMIGQMRDVVGAATAGQTYRSCMDSTVKYMFYKIPKSVQ 60

Qy 477 KRVTWYETWDSQRMDESLTKTLPTTVQLALAIQVNFIIISKVDLFGKCDTQMIYDM 536
Db 61 NRVTWYETWHSQGMDESELMVQLPKMRDLDAIDVNNIVSKVALFQCDRQMIYDM 120

Qy 537 LLRLKSVLYLPGDFVCKKGEGIKEMYIIKHGEVQVLGGPDGKTVLVTLKAGSVFGEISLL 596
Db 121 LKRLRSVYLPNDYVCKKGEGIKEMYIIQAQGVQVLGGPDGKSVLVTLKAGSVFGEISLL 180

Qy 597 AAGGNRRRTANVAHGFANLLTLDKKTLQELVHYPDSERILMKARVLLKQKAK 651
Db 181 AVGGNRRRTANVAHGFNTLFDLKKDLNEILVHYPESQKLLRKKARRMLRNNK 235

RESULT 5
US-09-842-758-75
Sequence 75, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A
APPLICANT: Malyankar, Uriel M
APPLICANT: Boldog, Ferenc L
APPLICANT: Zerhusen, Bryan D
APPLICANT: Spytek, Kimberly A
APPLICANT: Majumder, Kumud
APPLICANT: Tchernev, Velizar T
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esha A
APPLICANT: Smithson, Glennda
APPLICANT: MacDougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grosse, William M
APPLICANT: Edward, Szekeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591

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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-758-75

Query Match      20.1%; Score 850; DB 10; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNQSQOQTAAQENKGEESLKTKSTPVTSEEPHTNIQDKLSKNSSGDLTTNP 86
Db 5 NTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSEETS-- 43

Qy 87 DPQNAEPTGTVPROKEMDPKGEPNPQKPPAAPVINEYADAOQLHNLVKRMQRTALY 146
Db 44 ---SVLQP-GIAMEIRGLADSGQSFTGQ-----GIARLSRLIFLLRWAARH 87

Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYHYRLWLFVKVMPL 197
Db 88 VHQDQGFDPDFPRGAELKEVSSQESNAQANVGSEPADRG-----RSAW-----PL 136

Qy 198 -----TEYLKRIKLPSNI-DSYTDRLVLLMLLVLTAYNNWCWFIPRLVFPYQT 246
Db 137 AKCNTNTSNTTEBEKTKKDAIVDPSSNLYRWLTAIALPVFNWYLLICRACFDELQ 196

Qy 247 ADNIHYLIADIICDIYLDMLFIQPRLOFVRGGDIIVDSNELRKHRTSTFKQLDVAS 306
Db 197 SEYLMWLVLVDSADVLVLDVL-VRARTGFLEQGLMVSNTNRLMWHYKTTTQFKLDVLS 255

Qy 307 IIPFDICYLFPGFN-PMFRANRMLKYTSFFEPFNHLESIMDKAVIYRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLKVGTYNPEVRFNRLKSFRLFEPFDRTRTNYPNMFRIGNLVLYILIIH 315

Qy 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGGLPEPQTL 417
Db 316 WNACIYPAISKFIGFGTDSWVYPNISIPHEGRLSRKYIYSLYWSLTLTITIGETPPVKD 375

Qy 478 RVRTWYETWDSQRMDESLLKTLPTTVQALALADVNFSSIISKVDLFGKCDTQMIYDML 537
Db 436 RVIRWFDYLVWANKTVDEKEVLSPLDKLAEIAINVHLDTLKKVIRIQQCEAGLIVELV 495

Qy 538 LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVOVLGGDPDGTQKLVLTAKAGSVFGEISL 597
Db 496 LKLRPTVFSQDGIYCKKGDIGKEMYIINEGKLAUV-ADGVTQFVVLSDGSYFGEISILN 554

Qy 598 AGG---GNRRTANVVAHGFANLLTLDKKTLOEILVHYPSERILMKKAR-VLLKQK---A 650
Db 555 IKGSGKGNRRNTANIRSIGYSDLFCLSKDDLMALTEYPEAKKALEBKGRQILMKDNLIDE 614

Qy 651 KTAETATPPRKDALLFPPEKETPKLFTLLGGTGKASLARLL-----KLKREAAQK 702
Db 615 ELARAGADPKDL-----EKKVQLGSSL--DTLQTRFALLAEYNAQWKKQKRLSLE 666

Qy 703 KENSEGEE---EGKNEDEKQKNEDEKQK 728
Db 667 SOVKGGGDKPLADGEVFGATK-TEDKQK 694

RESULT 6
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US-09-855-828-14
; Sequence 14; Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CNGA1
US-09-855-828-14

Query Match      20.1%; Score 850; DB 11; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNQSQOQTAAQENKGEESLKTKSTPVTSEEPHTNIQDKLSKNSSGDLTTNP 86
Db 5 NTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSEETS-- 43

Qy 87 DPQNAEPTGTVPEQKEMDPKGEPNPQKPPAAPVINEYADAOQLHNLVKRMQRTALY 146
Db 44 ---SVLQP-GIAMEIRGLADSGQSFTGQ-----GIARLSRLIFLLRWAARH 87

Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYHYRLWLFVKVMPL 197
Db 88 VHQDQGFDPDFPRGAELKEVSSQESNAQANVGSEPADRG-----RSAW-----PL 136

Qy 198 -----TEYLKRIKLPSNI-DSYTDRLVLLMLLVLTAYNNWCWFIPRLVFPYQT 246
Db 137 AKCNTNTSNTTEBEKTKKDAIVDPSSNLYRWLTAIALPVFNWYLLICRACFDELQ 196

Qy 247 ADNIHYLIADIICDIYLDMLFIQPRLOFVRGGDIIVDSNELRKHRTSTFKQLDVAS 306
Db 197 SEYLMWLVLVDSADVLVLDVL-VRARTGFLEQGLMVSNTNRLMWHYKTTTQFKLDVLS 255

Qy 307 IIPFDICYLFPGFN-PMFRANRMLKYTSFFEPFNHLESIMDKAVIYRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLKVGTYNPEVRFNRLKSFRLFEPFDRTRTNYPNMFRIGNLVLYILIIH 315

Qy 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGGLPEPQTL 417
Db 316 WNACIYPAISKFIGFGTDSWVYPNISIPHEGRLSRKYIYSLYWSLTLTITIGETPPVKD 375

Qy 418 FEIVFQLLNFFSGVFVFSLLIGQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLQK 477
Db 376 EBYLFVVDVFLVGLVIFATIVGVNVSIMSNMNSRAEFQAKIDSIKQYMQFRKVTKDLET 435

Qy 478 RVRTWYETWDSQRMDESLLKTLPTTVQALALADVNFSSIISKVDLFGKCDTQMIYDML 537
Db 436 RVIRWFDYLVWANKTVDEKEVLSPLDKLAEIAINVHLDTLKKVIRIQQCEAGLIVELV 495

Qy 538 LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVOVLGGDPDGTQKLVLTAKAGSVFGEISL 597
Db 496 LKLRPTVFSQDGIYCKKGDIGKEMYIINEGKLAUV-ADGVTQFVVLSDGSYFGEISILN 554

Qy 598 AGG---GNRRTANVVAHGFANLLTLDKKTLOEILVHYPSERILMKKAR-VLLKQK---A 650
Db 555 IKGSGKGNRRNTANIRSIGYSDLFCLSKDDLMALTEYPEAKKALEBKGRQILMKDNLIDE 614

Qy 651 KTAETATPPRKDALLFPPEKETPKLFTLLGGTGKASLARLL-----KLKREAAQK 702
Db 615 ELARAGADPKDL-----EKKVQLGSSL--DTLQTRFALLAEYNAQWKKQKRLSLE 666

Qy 703 KENSEGEE---EGKNEDEKQKNEDEKQK 728
Db 667 SOVKGGGDKPLADGEVFGATK-TEDKQK 694

RESULT 6
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Db 615 ELARAGADPKDL-----EKKVEQLGSSL--DTLQTRFARLLAEYNATQMKMKQRLSQLE 666
Qy 703 KENSEGEE---EGKENEDKOKENEDKQK 728
Db 667 SQVKGKDKPLADGEVPGDATK-TEDKQK 694

RESULT 7
US-10-345-680-26
; Sequence 26, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING 34021, 44099, 25278,
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 62553, 302, 323,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM, ONNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-26

Query Match 20.1%; Score 850; DB 14; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHESNQSQQTAQENKGEKSLKTSPTVTSEPHNIOQKLSKKNSSGDLITNP 86
Db 5 NTQVSHES-----RTHLKVK-----TSRDRLNRAENGLSRAHSSEETS-- 43
Qy 87 DPQNAASPFTGTPVQKEMDPKGPSPQNPKPAPVINEVADALHNLVKRMQRTALY 146
Db 44 ---SVLPQ-GIATMETRGLADSGQSGFTGQ-----GIARLSRLIFLLRWARH 87
Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYRLWFKVKMPL 197
Db 88 VHQDQGPDPDFRFRGALKEVSSQESNAQNVGSQEPADRG-----RSAW-----PL 136
Qy 198 -----TEYLRKRLKPNIS--DSYTDRLYLWLLVTLVAYNWCWFPLRVPFYQT 246
Db 137 AKCNTNTSNTEEEKTKKDAIVVDFSSNLYRWLTAIALPVPFYNWLLICRACFDELQ 196
Qy 247 ADNIHYWLIADICDIIVLYDMLFIQPLQFVRGDIIVDSNELRKHYRTSTKFOLDVAS 306
Db 197 SEYLMMLVLDYSADVLVLDVL--VRARTGFEGLWGLWSDTNRLWQHKKITQPKLDVLS 255
Qy 307 IIPEDICYLFFGFN-PMFRANRMLKYTSFFEFNHLESIMDKAYIYRVRTTYLLFILH 365
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Db 256 LVPTDLAYLKGVTNYPEVRFNRLKFSRLFFDFDTETRTNYPNNFRIGNLVLYILIIH 315
Qy 366 INACVYVWASNYEGIGTTRWVVG-----EGNEYLRCCYVAVRTLITIGLPEPQTL 417
Db 316 WNACIYFAISXFIQGTDSWYFNIISPEHGRLSKYYISLYWSTLTTLTTIGETPPVKD 375
Qy 418 FEIVFQLNFFSGVVFSSLIQOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLQK 477
Db 376 EBYLFFVVDFLVGLVIFATIVGVNMGSMISNWNASRAEFQAKIDSIKQYMQPRKVTKDLET 435
Qy 478 RVRTWYETWDSORMLDESLLKLTPTVQIALAIDVNFISIISKVDLFGCDTQMIYDML 537
Db 436 RVIRMFYDLWANKTKVDEKVELKSLPDKLKAIAINVHLDLTKKVRIFQDCBAGLVELV 495
Qy 538 LRLKSLVLPDGFVCKGGEIGKEMVIIKHGVEVVLGGDTGKVLVTLKAGSVFGSISLLA 597
Db 496 LKLRPTVSPGDIYCKKGDIQKEMVIINEGKLVV-ADGVTQFVVLSDGSGVFGSISLN 554
Qy 598 AGG---GNRRTANVAVHGFANLLTLDKKTQLQEIIVHYPDSERILMKKAR-VLLKQK---A 650
Db 555 IKGSKSGNRRTANIRSIGYSLFCLSKDDLMEALTEYPEAKKALEEKGRQILMKDNLIDE 614
Qy 651 KTAETPPKDLALLFPKPEETPKLFTLLGGTGKASLARLL-----KUKRQAAQK 702
Db 615 ELARAGADPKDL-----EKKVEQLGSSL--DTLQTRFARLLAEYNATQMKMKQRLSQLE 666
Qy 703 KENSEGEE---EGKENEDKOKENEDKQK 728
Db 667 SQVKGKDKPLADGEVPGDATK-TEDKQK 694
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RESULT 8
US-10-174-333-75
; Sequence 75, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Raestelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsbrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
```

; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-333-75

Query Match 20.1%; Score 850; DB 15; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQOQTAAQENKEEKSLSKTSPTVTSSEPHNTIQDKLSKNSGDLTTNP 86
DB 5 NTQYSHPS-----RTHLVK-----TSDRLNRAENGLSRAHSSEETS--- 43

QY 87 DPQNAAEPTGTVPEQKEMDPGKEGNSPQKPPAAPVINEYADAQHLNFKMRQRTALY 146
DB 44 ---SVLQPG-GLAETRGADSGGSGFTGQ-----GIARLSRLIFLLRWAARH 87

QY 147 KKKLVGDLSSP-----RASPQAKPTAVPPVKESDDKPTHEYRLLFKVKKMLP 197
DB 88 VHHQDQGPDPFRFRGAELKEVSSQESNAQNVGQEPADRG-----RSAW-----EL 136

QY 198 -----TEVLKRLPNST-DSYTDRLYLLMLLTLAVNWCWFIPLRLVPPYQT 246
DB 137 AKCNTWTSNNTEEEKTKKDAIVDPDSNLRYRLMTALPVPFYNNYLLICACDFELQ 196

QY 247 ADNIHWLIADIICDIYLYDMLFIQPLQFVRGGDIIVDSNELRKHRTSTKFPQLDVAS 306
DB 197 SEYLMMLVLDYSADVLYVLDVL-VRARTGLEQGLMVSDTNRLWQHXYKTTQFKLDVLS 255

QY 307 IIPFDICYLFFGN-PMFPRANRMLKYSFPFNFHLESMDKAYIVRVIRTTGTYLLFILH 365
DB 256 LVPTDLAYLKVGNTYPEVRFNRLKFSRLFPFDPTRTETRTNYPNMFRIGNLVLYIILIH 315

QY 366 INACVYVWASNYEGIGTTRWYDG-----EGNEVLCRYVAVRTLITIGGLPEPQTL 417
DB 316 WNACIYFAISKFTGFGTDSWVYPNISIPHEGRLSRKIYISLYWSTLTLTIGTPPPVKD 375

QY 418 FEIVFOLLNFFSGVFSSLIQOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLQVK 477
DB 376 EEVLFVVVDVFLVGLVFIATVGNVGSWISNMNASRAEFQAKIDSIKQYMQFRKVTQDLET 435

QY 478 RVRTVEYTWDSORMLDESLLKTLPTTVOLALAIQVNFSSIISKVDLFGCDTQMTYDML 537
DB 436 RVIRWFDYLVWANKTKTDEKVELKSLPDKLKAETAINVHLDTLKKVIRIFQDCEAGLVELV 495

QY 538 LRLKSVLYLPGDPFVCKKGETGKEMYYIKHGEVOVLGGPDGTVLTKAGSVFGEISLLA 597
DB 496 LKLRPTVFGSDGIVCKKGGIGKEMYYINEGKLAV-ADGVTQFVVLSDGSYFGEISILN 554

QY 598 AGG---GNRRTANVVAHGFANLLTLDKKTLQELIHLVHPDSERILMKAR-VLLKQK---A 650
DB 555 IKGSKSGNRRTANIRSIGYSDLFCLSKDDLMEALTEYPEAKKALEEKGRIIMKDNLIDE 614

QY 651 KTAETAPPRKDALLLFPPEETKLPFKLLGGTGKASLARLL-----KLKREQAAQK 702
DB 615 ELARAGADPKDL-----EKKVQLGSSL--DTLQTRFARLLAEYNATQMKQKRLSQUE 666

QY 703 KENSEGGBE---EGKENEDKQKEDKQK 728
DB 667 SQVKGSGKPLADGEVPGDATK-TEDKQK 694

RESULT 9
US-10-029-677-16
; Sequence 16, Application US/10029677
; Publication No. US20030096249A1
; GENERAL INFORMATION:
; APPLICANT: Westphal, Ryan S.
; APPLICANT: Feder, John N.
; APPLICANT: Ramanathan, Chandra S.
; APPLICANT: Mintier, Gabriel A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
; TITLE OF INVENTION: POLYPEPTIDE
; FILE REFERENCE: D0187NP
; CURRENT APPLICATION NUMBER: US/10/029,677
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/257,865
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-029-677-16

Query Match 19.6%; Score 829; DB 14; Length 663;
Best Local Similarity 29.9%; Pred. No. 7.3e-52;
Matches 218; Conservative 132; Mismatches 283; Indels 96; Gaps 20;

QY 50 EKSLKTSPTVTSSEPHNTIQDKLSKNSGDLTTNPQNA--EPTGTVPEQKEMDPG 107
DB 3 EKANGVKSPANNHHPAPPAIKASGK---DHRASSRPQSAADTSSSELQOLAEMDAP 59

QY 108 KEGNSPQKPPAAPVINEYA-----DAQHLNFKMRQRTALYKKLVGDLSSPEA 160
DB 60 QQERGFRRIARLVGLREWAVNFRFEEPRDPSFLERFR-----GPEL 103

QY 161 SPQAKPTAVPPVKESDDKPTHEYRLLFKVKKMLPTEYLKRIKLPNSIDSYTDRLYLL 220
DB 104 HTVTTQQSGDKGDKDGEKGTKKPELF-----VLDPAGD-WYR 142

QY 221 WLLAVTL--AYNWCWFIPLRLVPEVPTADNIHWLIADIICDIYLYDMLFIQPLQFV 278
DB 143 WLFLIALPVLVNW-CLLV-ARACFSDLOKGYIYVWLVDYVSDVVIAD-LFIRLTGFL 199

QY 279 RGGDIIVDSNELRKHRTSTKFPQLDVASIIPEDICYLFFGF-NPMFRANRMLKYSFPFE 337
DB 200 EQGLLVKDTKLRDNVYIHTMQFKLDVASIIPTDLIYFAVGIHNPEVRFNRLHFARMFEF 259

QY 338 NHLESIMDKAVIYRVIRTTGTYLLFILHINACVYVWASNYEGIGTTRWY----DGE--- 390
DB 260 FORTETRTSYNIFRISNLILYIIIIHWNACIYAIKSGISGFGVDVTPYNNITDPEYG 319

QY 391 -GNEVLCRYVAVRTLITIGGLPEPQTLFEIVFOLLNFFSGVFVFSLLIGQMRDVIQAT 449
DB 320 LSREYICYLYWSTLTLTIGTPPPVKDBEYLFVIFDLIGLVLIPTAIIVGNVGSMLSNWN 379

QY 450 ANQNTFRACMDDTIAYMNNYSIPKLQVKRVRTWYEYTWDSQRMLEDSDLLKTLPTTVQLA 509
DB 380 ATAEAFQAKIDAVKHYMQFRKVKSEMAKVRWFYDLWTNKKSVDSREVLKKNLPAKLRAE 439

QY 510 LAIDVNFSSIISKVDLFGCDTQMTYDMLRLLKSVLYLPGDPFVCKKGETGKEMYYIKHGEV 569
DB 440 IAINVHLSTLKKVRIFQDCEAGLVELVTKRPQVSPGDIYCRKGDIGKEMYYIKEGKL 499

QY 570 QVLGGPDGTVLTKAGSVFGEISLLAAG---GNRRTANVVAHGFANILLTLDDKKTLOE 626
DB 500 AVV-ADGVTQYALLSAGSCFGEISILNIKSGKGNRTANIRSLGYSDL-FCLSKDDLME 558

QY 391 -GNEYLRCCYVAVRTLITIGGLPEQTLPEIYVQOLLNFFSGVVFSSLLIGQMRDVGAA 449
Db 320 LAREYICLYWSTLTLTTIGTPPPVVKDBEYLFVDFLIGVLIFATIVGNVGSIMSNW 379
QY 450 ANQNYPRACWDDTIAMNNYSIPKLVQKRVRTWYETWDSQRMDESLLKTLPTTVQLA 509
Db 380 AYRAEFQAKIDAVKHYMQFRKYSKMEAKVIRWFDYLTWTKKTVDERELKXNPAKRAE 439
QY 510 LAIDVNFISIISKVDLPFGCDTOMYDMLRLKSVLYLPDGFVCKKGEIKEMYIIKHGEV 569
Db 440 IATNVHLSTLKKVRIEHDCEAGLLVELKLRPQVSPGDIYCRKGDIGKEMYIIKEGKL 499
QY 570 QVLGGPDGTKVLVTLKAGSVGEISILAAG--GNRRTANVAHGAFANLLTLDKKTLOE 626
Db 500 AVV-ADGVTQYALLSAGSCFGGEISILNIGKSMGNRRRTANIRSLGYSDFCLSKDDLM 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE---ATPPRKDLALLFPKPEETPKLFTLLGTT 683
Db 559 AVTEYFPAKKVLEERGRELKMGELLDENEVATSMEDVDQEKLGQLETTNMTLYTRFG-- 616
QY 684 GKASLARLLKREQAQAKKENSEGEGEEBKENEKQEN--EDKOKENEDKQENED-- 739
Db 617 -----RL-----AETGAQOKLQKQRTVLETKMKQ-----NEDDY 648
QY 740 -KDKGREPEKPLDRP 754
Db 649 LSDGMNSPELAAADEP 664

RESULT 12

US-09-842-758-73
; Sequence 73, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Blma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: Macdougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-842-758-73

Query Match 19.4%; Score 820; DB 10; Length 732;
Best Local Similarity 28.8%; Pred.No. 3.8e-51;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

QY 24 SRNEEGSHPSNQSQOQTAAQENKGE-----EKSLTKTSPTVTSEEPHTNIQ 70
Db 32 YKRKWSGKGTQMSTQCESTRRAQTFCESNGHTWRMTEKSNVGVKSSPANN--HNNHV 88
QY 71 DKLSKNSGDLTTNPDQNAABPTGTVPEQK--EMDPKSGPNSPQKPPPAAPVINEYA 128
Db 89 PATIKANGKDESRTSRPQSAADDDTSELQRLAEMDAPQORRGFRIRIVLVGVIOWA 148
QY 129 -----DAQLHNLVKKRQRTALYKKLVGDLSSPEASPOKAPTAPVPVKESDDKPT 181
Db 149 NNFREEEARPDSEFLERFR-----GPELQTVTTQOGDKGDKDGGKGT 192
QY 182 EHYRLLMFKVKKMPLELYLKLPSNIDSYDRLYLWLLLVTL--AYNNNCWFPIPLR 239
Db 193 KKKFELF-----VLDPAGD-WYWRWLFVIAMPVLYNW-CLLV-AR 229
QY 240 LVFPYQTDANIHWLIADIICDIIVLYDMLFTQPLQFVRGGDIIVDSNELAKHYRTSTK 299
Db 230 ACFSDLQRGYFLVWLVDYFSDVVYIAD-LFIRLRTGLEQGLLVKDPKGLRDNVHTLIQ 288
QY 300 FOLDVASIIPEDICVYLFGEF-NPMFRANRMLKVYTFEFPNHHLESIMDKAYIRVIRTTG 358
Db 289 FKLDVASIIPDIIYFVAVGIHNPFLRNLHFAFMFEFFDRTEFTSYNIFRISNLVL 348
QY 359 YLLFIIHINACVYVWASNYEGIGTTRWVY---DGE---GNEYLRCCYVAVRTLITIGG 410
Db 349 YILVLIHWNACIYAIKSGISGFGVDTWVYPNITDPEYGLAREYIYCLYWSLTLTITIGE 408
QY 411 LPEQTLFPIVQLLNFFSGVVFSSLIQMRDVI GAATANQNYPRACWDDTIAMNNYS 470
Db 409 TPPPVKDEEYLFVDFLIGVLIFATIVGNVGSIMSNMNAEFOAKIDAVKHYMQFRK 468
QY 471 IPKLQKRVRTWYETWDSQRMDESLLKTLPTTVQALALADVNFISIISKVDLPFGCDT 530
Db 469 VKEMEAKVWKWFDYLTWTKKTVDEREVLKXNPAKRAEIANVHLSLTKKVRIFQDCEA 528
QY 531 QMIYDMLRLKSVLYLPDGFVCKKGEIKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVF 590
Db 529 GLLVVLVXLRPQVSPGDIYCRKGDIGKEMYIIKEGKLAVV-ADGVTQYALLSAGSCF 587
QY 591 GEISLLAAG--GNRRTANVAHGAFANLLTLDKKTLOELVHPDSEIRILMKARVLLK 647
Db 588 GEISILNIGKSMGNRRRTANIRSLGYSDFCLSKDDLMETYPDAKKVLEERGREL 647
QY 648 OKAKTAE---ATPPRKDLALLFPKPEETPKLFTLLGTTGKASLARLLKREQAQAKKE 704
Db 648 KEGLLDENEVAASMEVDVQEKLGQLETTNMTLYTRFG-----RL----- 687


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591 QY GEISLLAAG---GNRRRTANVVAHFANLLTLDKKTLQELIHYDPDSERILMKKARVLK 647
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
588 Db GEISILNIKSGMGNRRRTANIRSLGYSDFCLSKODLMEAVTEYPDAAKKVLEERGRIIM 647
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
548 QY QAKTAE---ATPRKDLALIFPPKEETPKLFKTLGGTGKASLARLLKLKREQAOKKE 704
    : : : : : : : : : : : : : : : : : : : : : : : : :
648 Db KEGGLDNEVAASMEVDVOEKLKOLETNWETLYTRFG-----RL----- 687
    : : : : : : : : : : : : : : : : : : : : : : : : :
705 QY NSEGESEBEGKENEDKOKEN--EDQKENEKGKENEKDKGREPEKPLDRP 754
    : : : : : : : : : : : : : : : : : : : : : : : : :
688 Db ----AETYGAOQLKQRITVLEVWKQNTÉ-----DDYLSDGWNSPAAAAEQP 732
    : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-174-333-73
; Sequence 73, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera S.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Curaseqelist version 0.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT

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; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-927-2

Query Match          19.4%; Score 819.5; DB 9; Length 664;
Best Local Similarity 29.5%; Pred. No. 3.6e-51;
Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;

Qy   50 EKSILKYSTPTVSEBHTNIQDKLSKNSSGDLTTNPDPQNAAEPTGTVEQK--EMDPG 107
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   3 EKTNGVKSSPANNHNHHA---PPAIKANGKDDHRTSRPHSAADDDTSSQLQRLADVAP 59

Qy   108 KEGPNSPONKPPAAPVINEYADAQLH-----NLVKRMQRTPALYKKKLVEGLDSSPEA 160
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   60 QQQRSGFRIRVLVGIIREWANKNFREPRDPSFLERFR-----GPGL 103

Qy   161 SPQTAKPTAVPPVKESDDKPTEHYRYLLMFKVKKMPLTEYLKRIKLPNSIDSYDRLYLL 220
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   104 QTVTTQGGDKGDGEDGTKKKFELF-----VLDPAGD-WYYC 142

Qy   221 WLLLVLT--AYNWNCFIPLRLVPFPOTADNTHYMLADIICDIYLYDMLFITQPRLQFV 278
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   143 WLFIAMPVLYNW-CULV-ARACFSLDQGYVLWLVDYSDVVVIAD-LFIRLRTGFL 199

Qy   279 RCGDIIVDSNELRKHYRTSTKFOLDVASIIPIDICYLFGFG-NPMFRANRMLKYTSFFEF 337
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   200 EQGLLVKDITKLRDNVIHTLKFLDVASIIPTDLIFYAVDIIHSPEVRFNLLHFARMFEF 259

Qy   338 NHLESIMDKAYIYRVIRTTGYLLFLHLINACYVYWASNYEGIGTRRWY----DGE--- 390
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   260 FDRTERTNYPNIFRISNLVILVIIHWNACTIYAISKSIKGFVDTWYVPIITDPEGY 319

Qy   391 -GNEYLCRCYVWARVTLLITIGGLPEPQTLFEIYFOLLNPFSGVFSSLIQOMRDVIGAAT 449
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   320 LAREYIYCYLWSLTIITLITIGETPPPVKDEYLFVFDLGLVLIIPATIIVGNVGSMLNNN 379

Qy   450 ANQNYFRACMDDTIAYMNYSIPKLQKRVRTWYEYTWDQSRLMDESDDLKLTLPITVQLA 509
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   380 ATRAEPQAKIDAVGHYMQPRKSKGMEAKVIRWFYDLWTNKKTVDEREILKNLPKLAKE 439

Qy   510 LAIDVNFSIISKVDLFKGCOTQMIYDMLRLKSLVLYLPGDFVCKKGEGIKEMYLIKHEGV 569
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   440 IAINVHSLTKKVRILPHDCAGLLVELVLKRPQVSPGDIYICRGKDIGIKEMYLIKKEGL 499

Qy   570 QVLGGPDGTKVLTCLKAGSVFGEISLLAAG---GNRRNTANVAHGFAALLTLDKKTLOE 626
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   500 AVV-ADDGVTVYALLSAGSCFGEISILNIKSGMKGNRRNTANIRSLGYSDLCLSKDLLWE 558

Qy   627 ILVHPYDSRIILMKARVLKKOKATAE---ATPPKOLALLFPKEETPKFLKILLGT 683
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   559 AVTEYPDACKVLEERGRELMEKGLLDENEVATSMEDVDVQEKLGULETNMETLYTRFG-- 616

Qy   684 GKASLARLLKLRQAAOKKENSEGEGEKNEKQKEN--EDKOKENEDKGENED-- 739
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   617 -----RLL-----AETYGAOQKLKQKITVLETWKQN-----NEDDY 648

Qy   740 -KDKGREPEEKPLDRP 754
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db   649 LSDGMNSPELAAADEP 664

Search completed: March 27, 2005, 21:27:19
Job time : 1174 secs

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Search completed: March 27, 2005, 21:27:19
Job time : 1174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 27, 2005, 20:25:22 ; Search time 51 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSAEGGBEVLTVIEVKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1952	46.1	909	2 S32538	cGMP-gated cation
2	1095	25.9	800	2 T19627	hypothetical prote
3	834.5	19.7	695	2 S74179	cyclic nucleotide-
4	829	19.6	663	2 S11521	cAMP-gated channel
5	821.5	19.4	735	2 I50630	alpha subunit of c
6	820	19.4	732	2 S35691	cyclic nucleotide-
7	819.5	19.4	688	2 B42161	cGMP-gated cation
8	818.5	19.3	690	2 A42161	cGMP-gated cation
9	818	19.3	686	1 A48482	cGMP-gated ion cha
10	807.5	19.1	682	1 JH0560	cyclic nucleotide-
11	804	19.0	664	2 S11517	cyclic nucleotide-
12	801.5	18.9	691	2 J66509	rod cyclic nucleot
13	797	18.8	690	1 S07103	cGMP-gated ion cha
14	794	18.8	706	2 A52551	cyclic nucleotide-
15	771	18.2	645	2 I50680	alpha subunit of r
16	770	18.2	772	2 S28292	hypothetical prote
17	718	17.0	665	2 S52072	DmGNC protein - f
18	640	15.1	575	2 I59327	olfactory cyclic n
19	555	13.1	673	2 T20936	hypothetical prote
20	530	12.5	611	2 T20935	hypothetical prote
21	484	11.4	261	2 I78559	cyclic nucleotide-
22	476	11.2	261	2 I78560	cyclic nucleotide-
23	441.5	10.4	644	2 T33125	hypothetical prote
24	366.5	8.7	767	2 T21969	hypothetical prote
25	349	8.2	828	2 T52045	potassium channel
26	349	8.2	962	2 I53197	potassium channel
27	336	7.9	989	2 I48912	potassium channel
28	331.5	7.8	807	2 T12177	potassium channel
29	323.5	7.6	845	2 T07052	probable potassium

30	321	7.6	688	2 S55349	potassium channel
31	318	7.5	787	2 S68699	potassium channel
32	317.5	7.5	1159	2 I38465	probable potassium
33	314	7.4	883	2 T07651	potassium channel
34	313.5	7.4	662	2 T04461	potassium channel
35	311	7.3	887	2 T03939	potassium channel
36	302.5	7.1	838	2 S23606	potassium channel
37	302.5	7.1	857	2 S62694	potassium channel
38	296	7.0	934	2 T42394	potassium channel
39	292	6.9	1174	2 A40853	potassium channel
40	287	6.8	716	2 T51354	cyclic nucleotide-
41	284	6.7	706	2 T51432	cyclic nucleotide-
42	282	6.7	880	2 F85381	potassium channel-
43	282	6.7	916	2 T05360	probable potassium
44	280	6.6	702	2 T04424	probable calmoduli
45	278.5	6.6	718	2 G84902	hypothetical prote

ALIGNMENTS

RESULT 1

S32538
cGMP-gated cation channel 2, rod - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: S32538
R:Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.
Nature 362, 764-767, 1993
A:Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.
A:Reference number: S32538; MUID:93226050; PMID:7682292
A:Accession: S32538
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-909 <CHE>
A:Cross-references: UNIPROT:O43636
C:Keywords: cGMP binding
F:620-742/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 46.1%; Score 1952; DB 2; Length 909;
Best Local Similarity 46.4%; Pred. No. 2.9e-112;
Matches 405; Conservative 121; Mismatches 237; Indels 110; Gaps 18;

Qy	14	IGENNEEQSRNEEGSHPSNQQTAAQ--ENKGE---EKSLTKTSTVTSEEPHTN 68
Db	67	VGEAAKKEAEKAEAEAEVAEEAEKPEQDAETKEEPEAEAEAAAGSGVPATKQHPVQ 126
Qy	69	IQDK-----LSKNSSGDLTTNPDPQNAAEPTGTVPQKEMDPGKEGPN----- 112
Db	127	VEDTDADSCPLMAEENPPS--TVLPFSPAKSDTLIVPSSASGTHRKKLPSEDEAEELK 184
Qy	113	--SPQNKP-----PAAP-----VINEYADAQLHNLVKRMORTALY 146
Db	185	ALSPAESPVVAMSDPTTKDTGDQDRAASTASTNSALIND----RLQELVKLFKERTKV 240
Qy	147	KKKLVEGDLS----SPEASPTAKPTAPVPVKESDDKPT--EHYVRLLMFKVKMPLTEY 200
Db	241	KEKLIDPVTSDSESPKSPAKAPEADPTKPAEAPVEEHEHYCDMLCCFKHPRWKY 300
Qy	201	LKR1KLNSIDSYTRLYLLMLLVLAYNNWCNFIPLRLVFPYQTDADNIHYWLIADIIC 260
Db	301	---QFQSIDPLTNLMYLVLMFFVMAWNNWNCWLIIPVRWAFPYQTDPNIHLLMLDYL 356
Qy	261	DIIVLYDMLFQPLQFVRGDIIVDSNELRKHRTSTKTFOLDVASIIPFCIVLFGFN 320
Db	357	DLIYFLDITVFQTLQFVRGDIITDKDMNNYLNKRRFKMDLLSLPLFLYLKVGVN 416
Qy	321	PMFRANMLKYSFFEFNNHLESIMDKAYIVRVIRTTGYLILFILHINACVYVWASNEGI 380
Db	417	PLRLPCLCKYMAFEFNSRLSILSKAYVTVRTTAYLLYSLHNSCLYVWASAYQGL 476
Qy	381	GTTRWVYDGEENYLCRYNAVRTLITIGGLPEPQTLFEIVFQLLNFPFSVGVFSSLIQ 440

Db 477 GSTHWYDGVGNSYRCYYFAVKTLITIGLPPDKTLFIIVFOLLNYFTGVFAFVMIQ 536

QY 441 MRDVI GAATANQNYFRACMDTAYWNNYSIPKLVQKRVPTWYETWDSQRMLEDSDLLK 500

Db 537 MRDVGAATAGQTYRSCMDSTVKYWNFYKIPKSVQNRVKTWYETWHSQGLMDESELMV 596

QY 501 TLPPTVQLALAIQVNFSSISKVOLFQKCDQMTIYDMLLRKLSVLYLPQDFVCKKGBIGKE 560

Db 597 QLPDKWRLDLAIQVNNIVSKVALFQCDQMTIYDMLLRKLSVLYLPQDFVCKKGBIGRE 656

QY 561 MYIIKHGEVOLGPDGDKVLTAKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLD 620

Db 657 MYIIQAGVQVGLGPDGKSVLTLKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLD 716

QY 621 KKTLORTLVHPDSEIRILMKARVLKQAKTAETAPPRKDLALLPPKKEETPKLFTLL 680

Db 717 KDLNEILVHPYSEKLLRKAARMRLSNK-----PKEEKSVLLIAPPRAAGTPKLFNAAL 771

QY 681 GGTGKAS-----LARLLKREQAQKENSEGEGEKENEDKQENEDKQ 728

Db 772 AMTKWGGKAGKGLAHLRLKELALEAAKQDEL---VEQAKSSQDVKGEGSAAP 828

QY 729 ENEDKQKE-NEDKDKGREPEKP-----LORPECTASPIAVEEPHPSVRRTVLP 776

Db 829 DQHTHPKEAATDPPAPRTPEPPGSPSPASLGRPEGEERGPA-EPEHSVR-----882

QY 777 RGTSRQSLIISMAPSAEGGEVLTIEVKEKAKQ 809

Db 883 -----ICMSFGPEPGEOILSVKMPEREE 906

RESULT 2

T19627

hypotheical protein F36F2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19627; T21863

R;Kershaw, J.

submitted to the EMBL Data Library, April 1997

A;Reference number: Z19153

A;Accession: T19627

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-800 <W12>

A;Cross-references: UNIPROT:O62237; EMBL:Z93778; PIDN:CAB07847.1; GSPDB:GN00019; CBSP:F36F2.5

A;Experimental source: Clone C31H5

R;Cottage, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19479

A;Accession: T21863

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-800 <W12>

A;Cross-references: EMBL:Z81532; PIDN:CAB04328.1; GSPDB:GN00019; CBSP:F36F2.5

A;Experimental source: clone F36F2

C;Genetics:

A;Gene: CBSP:F36F2.5

A;Map position: 1

A;Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1; 56

Query Match 25.9%; Score 1095; DB 2; Length 800;

Best Local Similarity 31.9%; Pred. No. 1.3e-59;

Matches 258; Conservative 153; Mismatches 301; Indels 98; Gaps 22;

QY 2 FKSLSKVNKYKPIGNNENQSGRRNEG---SHPNQSQQTAAQENKGEESKLTKTST 59

Db 21 FSVVDQKASKPT-QLSEKWKSPRSDPSDLLDPANAS-----KEPSASTRPL 68

QY 59 PV-TSEPHNTIQDKLSKNSSGDLTNP-----DQNAAEPTGTVPEQKEMDPGKEGN 112

Db 69 FYPPTRPPEVQI-----DEVESPLIGLIDETDDHLDG-----RLDPAASFDA 113

QY 113 SPQNKPPAAPVINEYADAQ-----LHNLVKMRQRTALYKKKLVEGLDSSPEASPT 164

Db 114 NSLSATRASSIIEDDVRSQISFIMRERLHSAIAKVRHRTSAVREDLIR---ETPEDTVSM 170

QY 165 AKPTAVPPVKESDDKPTHEHYLLWFKVK-KMPLFEYLR---IKLPNSIDSYDRLYLL 220

Db 171 A--SNVP--KQNEHRPS--LMSLIGLQNRSESPVDTVKNCFGFSLKGTGFHPY-GRFYMT 223

QY 221 WLLVTLAYNMNCWFIPLRVPPYOTADNIHYWLIADIICDIIYLYDMLFIOPRLQFVRG 280

Db 224 WLSLVTLCFLPNAFCIPLRSSYPYQADNMWTFWFDVYSCDLVYVIDMLLILKPLRAFTRG 283

QY 281 GDIIVDSNELRKHYRTSTKFDLDVASIIPDFICYLFFGFNPMFRANRMLKYTSFFFNHH 340

Db 284 GIOVKIYKDTQRHYLMTRTFKLDLILSILPTDLMYFFGKMPIWRINRVLKINSFWLLFDM 343

QY 341 LESIMDKAVIYRVIRTTGYLLFILHINACVYWASNYEGIG-----TTRVYDYG 389

Db 344 LNSFANPYAIRARTLSYMIYIIHCNSCVYKLSALQAFQIAYLENGKWYLNKWVYNN 403

QY 390 EGNEYLRVCYVAVRTLITIGLPEPQTLFEIVFOLLNFFSGVFFSSLIGQMRDVIQAAT 449

Db 404 QGNAYIRCFYTAATATSTGNNPAPTNIYIEIYMTCSWMMGVFVPALLIGQIRDIVSNAN 463

QY 450 ANQNYFRACMDDTIAYMNNYSIPKLVQKRVPTWYETWDSQRMLEDSDLLKTLPTTVQLA 509

Db 464 RNREEFORKMDLALGCEKGLKMETNTRVDFIYTWQOQKTLDKELIPLKLQTD 523

QY 510 LAIDVNFSSIISKVDLPKGCQTQMIYDMLLRKLSVLYLPQDFVCKKGEIKEMVLIKHGEV 569

Db 524 LALSVDYTLTKSVQLFQDCDRALLRDLVLKRPVFLPGDMICLKGDGVKEMVIYINQGL 583

QY 570 QVLGPGDKVLVTLKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLDKKTLEIIV 629

Db 584 QVGGDHNEKIFAELAQAVFGEISLAAAGGNRRRTASIRAKGYCTFLVLAKEDLNDVIR 643

QY 630 HYPDSEIRILMKARVLKQAKTAETAPPRKDLALL-----PPPKEETPKLFTLLGGT- 683

Db 644 YYPQAQTLRRKAAAMLKNDKSKDEKTEKIKQAQAELEDCKINPR-QVPEKLIITLIANMTE 702

QY 684 -----GKASLARLLKREQAQK-----ENSEGEGEKENEDKQENED-----725

Db 703 MNENKGVQELKKVIEETEKSRRQSIYYPWSTLQRDDDEEWNDEEDSLDVGEDFDLP 762

QY 726 -KQKNEEDKGENEDKDKGREPEEKPLDRP 754

Db 763 TNHSDDED---PMEDVDLAPEVHDDWDQF 789

RESULT 3

S74179

cyclic nucleotide-gated channel protein - human

C;Species: Homo sapiens (man)

C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999

C;Accession: S74179

R;Yu, W.P.; Grunwald, M.E.; Yau, K.W.

FEBS Lett. 393, 211-215, 1996

A;Title: Molecular cloning, functional expression and chromosomal localization of a human

A;Reference number: S74179; MUID:96409310; PMID:8814292

A;Accession: S74179

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-695 <YUW>

A;Experimental source: retina

C;Genetics:

A;Map position: 2

C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-

C;Keywords: ion channel; ion transport; membrane protein

F;482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.7%; Score 834.5; DB 2; Length 695;

Best Local Similarity 29.7%; Pred. No. 1.2e-43;

Matches 223; Conservative 149; Mismatches 271; Indels 107; Gaps 22;

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27 NEEGSHPSNQSQTTAEENKEBKSUKTKSTPTVTSBEPHTNIQDKLXKNSSGDLTNP 86
   : : : : :
5 NTOYSHFS-----RTHLEVTSDRLNRAENGLSRAHSSSEETS-- 43
   : : : : :
87 DPQNAAEPTGTVPEKEMDPKEGPNSPONKPPAAPVINEYADAOHLNLVKEMRQRTALY 146
   : : : : :
44 ---SVLPQ-GIAMETRLGADSGQSFTGQ-----GIARLSRLFLFLRWRARH 87
   : : : : :
147 KKKLVEGDLSPP-----EASPOQAKTAPVPPVKESDDPKTEHYRYRLWFKVKMPL 197
   : : : : :
88 VHHQDQGPDSPPDRFRGAELKEVSSQESNAQANVGSQEPADRG-----RSAN-----PL 136
   : : : : :
198 -----TEYLKRIKLPNSI--DSYTRDRLYLWLLVTLAYNNWCWFPLRLVPFYQT 246
   : : : : :
137 AKCNTNTSNNTBEEKTKKKDAOIIVDPSSNLYYRWLTAIALPVFNNWYLLITCRACFDELQ 196
   : : : : :
247 ADNTHYWLIIADICDIIYLYDMLFIQRLQPVRCGDIIVDSNELKRVHRTSTKPOLDVAS 306
   : : : : :
197 SEYLMWLWLDYSADVLYVDLVL--VRATGLEQGLMWSDTNRLWQHYKTTQPKLDVLS 255
   : : : : :
307 IIPEDICYLFFGFN--PMFRANRMLKYTSFFEFNHLESIMDKAYIVRVIRTTGYLLFILH 365
   : : : : :
256 LVPDTLAYLVKVTGYPEVRFNRLLKFSRLFEFFDRTETRINYPNMFRIGNLVLYILIIH 315
   : : : : :
366 INACVYTWASNYEGIGTRWYDG-----EGNEYLRCYVAWRTLIITIGLPEPOTL 417
   : : : : :
316 WNACIYPAISKFIQFGFDWSVYPNISIPEHGRLSRKVIYSLWSTLTLTTIGETPPPVKD 375
   : : : : :
418 FEIVFOLLNPFSGVVFVSSLIGQMRDVI GAATANQNYFRACMDDTIAMNNYSIPKLVOK 477
   : : : : :
376 EYLFVVVDVLVGLVLI FATIVGNVGSIMNNASRAEFQAKIDSIKOYMOFRKVTKDLET 435
   : : : : :
478 RVRTWYBYTWDQSQRLDESOLLKPLTPVQLALADIVNFSTIISKVDLPKGCOTOMIDML 537
   : : : : :
436 RVIRWPDFLWANKTVDEKEVILSLPKLKAELAINVHLDTLKVRFPQDCEAGLIVELY 495
   : : : : :
538 LRLKSVLYLPQDVFCKGETGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLA 597
   : : : : :
496 LKLRPTVSPGDYICKKGIDGKEMYIINEGKLAVV--ADDGVTQFVVLSDGYSFGEISILN 554
   : : : : :
598 AGG---GNRRTANVVAHFANILLTDKKTLOEILVHPY--DSEIRILMKAR-VLLKQK--- 649
   : : : : :
555 IGKSGSGNRRTANIRSIGYDLCFLSKDDLMLEALTEYPGQAKKALEBKRGQILMKOWLID 614
   : : : : :
650 AKTAEAETPPRKDALLFPPEKEETPKFKTLGGTGKASLARLL-----KLKREOAAQ 701
   : : : : :
615 BELARAGADPKDL-----BEKVQLGSSL--DTLOTRFARLLAEYNATQWKKQRLSQL 666
   : : : : :
702 KKNSEGEET-----EGKNEKDQKENEKDQK 728
   : : : : :
667 ESQVKGGGDKPLADGEVPGDATK--TEDKOO 695
   : : : : :

```

RESULT 4
 S11521
 CAMP-gated channel protein - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S11521
 R;Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B.
 FEBS Lett. 270, 24-29, 1990
 A;Title: Primary structure of cAMP-gated channel from bovine olfactory epithelium.
 A;Reference number: S11521; MUID: 91032022; PMID:1699793
 A;Accession: S11521
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-663 <LUD>
 A;Cross-references: UNIPROT:Q03041; GB:X55010; NID:g287743; PIDN:CAA38754.1; PID:g287744
 C;Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide
 F;454-578/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
 Query Match 19.6%; Score 829; DB 2; Length 663;
 Best Local Similarity 29.9%; Pred. No. 2.4e-43;

Matches 218; Conservative 132; Mismatches 283; Indels 96; Gaps 20;	
Qy	50 EKSLKTSPTVTSSEPHNTIODKLSKKNSSGDLTTNPDQNA--EPTGTVPEQKMDPG 107
Db	3 EKANGVSSPANNHHHAPPAIKASGKD---DHRASSRPOSAAADDTSSSELQQIAEMDAP 59
Qy	108 KEGNSPQNKPPAAPVINEYA-----DAQLHNLVKRMORTALYKKKLVEGDLSLSPA 160
Db	60 QQRGGGFRFARLVGVLRWAYRNFRSEEPDPDSFLERF-----GPEL 103
Qy	161 SPQAKPTAVPPVKESDDKTEHYHYLLFWFKVKOMPLTEYLKRIKLPNSIDSYDRIYLL 220
Db	104 HTVTTQCGDKGDKGEGKGTKKKEFELF-----VLDPADG-WYR 142
Qy	221 WLLVLT--AYNWCWFIPLRVLPPYQTDADNIHWLIADIICDIYLYDMLFIQPRLOFV 278
Db	143 WLFIALFVLVNW-CLLV-ARACFSDIQKGYIIVWLVDVSDVVYIAD-LFIRLRGFL 199
Qy	279 RGGDIIVDSNELRKHYSSTKFOOLDVASIIPFDICYLFFGF-NPMFRANMLKYTSFEF 337
Db	200 EQGLLVKDTKRLRNYIHTQFKLDVASIPTDLIYFAVGHNPEVFNRLHLPARMFEF 259
Qy	338 NHHLESIMDKAYIRVIRTTGYLLFIHLINACVYVWASNYEGIGTTRWY----DGB--- 390
Db	260 PDRTEITSVPNFRISNLIIYLIILIIHWACIYALSKSIGFVDVTWVYPTNIDTDPGY 319
Qy	391 -GNEYLRCYWAVRTLITIGGLPEPOTLFEIVFOLLNFFSGVFSSLIQOMRDVIGAA 449
Db	320 LSREVIYLYWSTLTLTIGETPPVKDEEVLVIFDFLGLVIFATIVGVNVSMTNMN 379
Qy	450 ANQYFRACMDDTIAYNNYSIPKLVQKRVRTWYETWDSQRMDESLLKTLPTTVOLA 509
Db	380 ATRAEPQAKIDAVKHVYQFRKVKSEMAKVIKWFYDLWTNKSVDREVLKNLPKLRAR 439
Qy	510 LAIDVNSIISKVDLPKGCOTQMIYDMLBLKSVLYLPQDFVCKKGKIGKEMIIKGEV 569
Db	440 IAINVHLSTLKVRIFQDCAGLLVELVLKLRPQVSPGDIYCRKGDIGKEMIIKEGKL 499
Qy	570 QVLGGPDGTVLVTLKAGSVFGRISLLAAG---GNRRTVANVAHGPFANLLTLDKKTLOE 626
Db	500 AV--ADGVTVQYALLSAGSCFGRISILNIKSGKMGNNRRTANIRSLGVDLFCLSKDDLME 558
Qy	627 ILVHPDSEIRILMKARVLKQAKTAE---ATPPRKDALLPPPKETPKLPKTLGGT 683
Db	559 AVTEYPAKRVLBERGERIILMKGLLDENEVAASMEVDV-----QKLEQLETNM--DT 610
Qy	684 GKASLARLKLKREQAQAACKENSEGGEKENEKOKEN--EDKOKENEDKGENEDKD 741
Db	611 LYTFARLL-----AEBYTAQQKLKQIRIVLETKMKQNNEDDSLSDGMN 654
Qy	742 KGREPEPK 750
Db	655 SPPEPAEKP 663

```

RESULT 5
150630
alpha subunit of cone photoreceptor CNG-channel - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50630
R/Bonight, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; K
Neuron 10, 865-877, 1993
A/Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated
A/Reference number: I50630; MUID:93264082; PMID:7684234

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A/Accession: I30650
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-735 <BON>
A/Cross-references: UNIPROT:Q90805; EMBL:X89598; NID:g90850; PIDN:CAA61757.1;
F/534-648/Domain: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nu
F/534-648/Domain: CAMP receptor protein cyclic nucleotide-binding domain homolo

Db 3 LSMKTNIIINWHISFVNIPNVIIPAIKEIRRMENGACSFSDDDN-----GSLSESENE 57
Qy 106 PG-----REGPNSPQKPPAARV---INEYADAQLHNLVKRMQRORTALYKXKLVGEGD 154
Db 58 DSFPFRSNVYKRGPSQREQLPGTWTALFNVNSSNKDQEPKXKXKK-----EKSKADD 113
Qy 155 LSSPASQOTAKPTAVPPVKESDDKPTTHYRLLWFKVKOMPLTYLKRILKILPNISIDSYT 214
Db 114 KNEKKDPEKXKXKE-----KEKEKXKXKE-----KTKEKEKEKEKEVWIDPSGNTYY 162
Qy 215 DRLVLLWLLVTL--AYNWCNCFILRLVFPYQADNIHMYLIADICDIIYLYDMLFIQ 272
Db 163 N-----WLFCTLPWYNT--MIARACFDELQSDYLEWLIIFYNSNVVLADM--FVR 214
Qy 273 PRQVQRGGDIIVDSNELKRYSTKQFDVASIIPFDICYLPFGFN--PMFRANRMLKY 331
Db 215 TRTGVEQGLLVKDRMKLIEYKANKLQKLDVLSVPTDLYIKFGWNYPEIRLNRLRI 274
Qy 332 TSFPEFNHLSIMDKAYIYRVITGTYLLFILHINACVYVWASNYEGIGITRWY---- 387
Db 275 SRMFEFFORTTETRTNYNPIFRISNLVMIYIIHWNACVYYSISKAIFGNDTWYYPDVN 334
Qy 388 DGE-----GNEYLRCYVAVRTLITIGLPEPQTLPEIVFQLLNFFSGVVFSSLIQMRD 443
Db 335 DPEFGLARKVYSLYWTLTITIGETPPVLDSEYIFVVDVFLIGLIFATIVGNIGS 394
Qy 444 VIGATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYETWDSQRMDESLLKTLTP 503
Db 395 MISNNAARAEFQSRVDAIKQYMFNRVNSKDMKEVWKWFDYLTWNTKKTVDEREVLRLP 454
Qy 504 TVVQLALAIQVNFISIKVDLFGCDTQMIYDMLRLKSVLYLPDGFVCKGKEIGENYI 563
Db 455 DKLRAEIAINVHLDLTKVRIFADCEAGLLVELVLKLPQVYSPGDYICKGDIIGREMYI 514
Qy 564 IKHGEVQVGGPDGKVLVTLKAGSVGEISILAAAG--GNRRTANVAVHGFANLLTLD 620
Db 515 IKEGKLAVV--ADDGTTQVFLVSDGSYFGEISILNIGSKAGNRRTANIKSIGYSDLFCLS 573
Qy 621 KKTQEIILVHPDSEIRILMKARVLL 646
Db 574 KDDLMEVLTEYPDAKTWMLEEKGRQL 599
RESULT 8
A42161
cGMP-gated cation channel, rod photoreceptor - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A42161
R:Pittler, S.J.; Lee, A.K.; Althert, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa
J. Biol. Chem. 267, 6257-6262, 1992
A:Title: Primary structure and chromosomal localization of human and mouse rod photorece
A:Reference number: A42161; MUID:92210603; PMID:1372902
A:Accession: A42161
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-690 <PIT>
A:Cross-references: UNIPROT:P29973; GB:M84741; NID:gl80461; PIDN:AAA52010.1; PID:gl80462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cGMP binding; transmembrane protein
F:479-603/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 19.3%; Score 818.5; DB 2; Length 690;
Beat Local Similarity 30.0%; Pred. No. 1.1e-42;
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;
Qy 5 LTKVNVKVPIGENNENEOSSRRNEEGSHPS-----NQSQQTAAQENKKEE-----KSL 53
Db 17 VTMPNVIVP-----DIEKEIRRMENGACSFSDSDSAYTSEENENPHARGSFYSYSL 71
Qy 54 KTKSTPTVTSBPHTNIQDKLSKSSGDLTTNPPDQNAABTGTVPQEKMDPKGEGNS 113
Db 72 R-KGGPSQREQLFCATAIFNVNNS-----NKD-----QEPEEKKKKKKKKSDDKNE 121

Qy 114 POKPPAAPVINEYADAQLHNLVKRMQRORTALYKXKLVGEGDSSPEASPOKAPTAVPPV 173
Db 122 NKNDPE-----KXKXKXKXKXK-----E 141
Qy 174 KESDDKPTHEHYRLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLLYLLMLLVTL--AYNW 231
Db 142 EKSKDKKEHH-----KKEVVV-----IDP-SGNTYNNWLFCTILPVMYNNW 180
Qy 232 NCWFILRLVFPYQADNIHMYLIADICDIIYLYDMLFIQPRLOQVVRGGDIIVDSNELR 291
Db 181 T--MVIARACFDELQSDYLEWLIYVSDIVYLLDM--FVTRTGYLEQGLLVKBELKLI 237
Qy 292 KHYRTSTKQFDVASIIPFDICYLPFGFN--PMFRANRMLKYTSFPEFNHLSIMDKAYI 350
Db 238 NKYSKNLQKLDVLSIPTDLYIKFGWNYPEIRLNRLRFSRMFEFFORTTETRTNYENI 297
Qy 351 YRVITGTYLLFILHINACVYVWASNYEGIGITRWY----DGE-----GNEYLRCYVAV 402
Db 298 FRISNLVMIYIIHWNACVYYSISKAIFGNDTWYYPDINDPFBFGLARKVYVSLYWS 357
Qy 403 RLTITIGLPEPQTLPEIVFQLLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDDT 462
Db 358 LTLTIGETPPVLDSEYIFVVDVFLIGLIFATIVGNIGSMISNNAARAEFQARIDAI 417
Qy 463 IAYMNNYSIPKLVQKRVRTWYETWDSQRMDESLLKTLPTTVQLALAIQVNFISIKV 522
Db 418 KQYMFNRVNSKDMKEVWKWFDYLTWNTKKTVDKEVLYLPDKLRAEIAINVHLDLTKV 477
Qy 523 DLFGCDTQMIYDMLRLKSVLYLPDGFVCKGKEIGENYI IKHGEVQVGGPDGKTVLV 582
Db 478 RIFADCEAGLLVELVLKLPQVYSPGDYICKGDIIGREMYI IKGKLAVV--ADDGVTQFV 536
Qy 583 TLKAGSVGEISILAAAG--GNRRTANVAVHGFANLLTLDKKTLOETLVHVPDSEIRILM 639
Db 537 VLSQDSTFGEISILNIGSKAGNRRTANIKSIGYSDLFCLS KDDLMELTETYPDAKTWMLE 596
Qy 640 KKAARVLLKQKA---KTAEATPPRKDLALLPPPKKEETPKLFPKTLIGGTGKASLARLL--- 692
Db 597 EKGQILMKQGLLDLNIANAGSDPKDLEEKVTRMEGSDVLLQOT-----RPARILAEY 648
Qy 693 -----KUKREQAOKK 703
Db 649 ESMQQLKQRLTKVEK 664

RESULT 9

A44842

cGMP-gated ion channel protein - human

N:Alternate names: rod photoreceptor cGMP-gated channel

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A44842

R:Dhallan, R.S.; Macke, J.P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nathans, J.

J. Neurosci. 12, 3248-3256, 1992

A:Title: Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure

A:Reference number: A44842; MUID:92356211; PMID:1379636

A:Accession: A44842

A:Molecule type: mRNA

A:Residues: 1-686 <DHA>

A:Cross-references: GB:S42457; NID:g252853; PIDN:AAB22778.1; PID:g252854

A:Experimental source: retina

A>Note: sequence extracted from NCBI backbone (NCBIN:110250, NCBI:P:110251)

C:Genetics: intron positions were determined from genomic sequence

A:Gene: GDB:CNCG1; CNCG

A:Cross-references: GDB:127557; OMIM:123825

A:Map position: 4p14-q43

A:Introns: 36/2; 75/2; 95/2; 110/2; 146/2; 182/2; 218/2

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-

C:Keywords: cGMP binding; eye; ion channel; ion transport; retina; transmembrane protein

F:475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match		19.3%; Score 818; DB 1; Length 686;
Best Local Similarity		25.9%; Pred. No. 1.2e-42;
Matches		226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;
Qy	5	LTKNVKYKPTGENNENQSRNREGSHPS-----NQSQQTQAQENKGE-----KSL 53
Db	13	VTMPNVIVP-----DIEKEIRRMENGACSFSEDDDSASTSESESENPHARGSFYSKSL 67
Qy	54	KTKSTPTVTSBEPTNIGDKLSKNSSGDLTTNPPQNAAPTGTVPQKMDPKGKGPNS 113
Db	68	R-KGPPSQRQYLPQALAFNVNNS-----NKD-----QEPKPKKKKKKKSKDNKNE 117
Qy	114	PONKPPAAPVINEYADQLHNLVKRMQRORTALYKKLVEGDLSSPEASPTAKPTAVPPV 173
Db	118	NKNDPE-----KXKKKKDKKKKK-----E 137
Qy	174	KESDDKTEHYRYLLWFKVKKMPLETEYLKRIKLPNSIDSYTDRLYLWLLLVTL---AYNW 231
Db	138	EKSOKKKEE-----KKEVV-----IDP-SGNTYNNWLCITLPVWYNW 176
Qy	232	NCWFIPRLVFPYQTADNIHYLLADIICDIILYDMLFIQPRLOFVRGGDIIVDSNELR 291
Db	177	T--WVIARACFDELQSDYLEWLLIDVSDIVLIDM-FVTRTGYLEQGLLVKEELKLI 233
Qy	292	KHYRTSTKFOLDVASIIPFDICVLPFGFN-PMFRANRMLKYTGFFEPNHHLESIMDKAYI 350
Db	234	NYKSNLQFKLDVLSIPTDLLYFKLGWNYPEIRLNELLRFSRMFEPFQRTETRTNYPNI 293
Qy	351	YRVIRTTGYLLFILHINACVYVWASNYEGIGTRTWY-----DGE-----GNEYLRCYWAV 402
Db	294	FRISNLVMIYVIIHWNACVYFYSISKAGFGNDTWVPYDINDPEFGRLARKYVYSLYWST 353
Qy	403	RTLITIGLPEPQTLPEIYFQLLNFPFSGVVFSSLIGOMRDVIGAATANQNYFRACMDDT 462
Db	354	LTLTTIGETPPVRDSYVFWVDLIGVLIFATIVNGISMLSNMNAARAEQARIDAI 413
Qy	463	IAYMNNYSIPKLQKRVRTWYETWDSORMLDESLLKTLPTTVQLALAIQVNFISIISKV 522
Db	414	KQYHPRNVSKMEKRVIKFDFYLTWTKVTDEKVLKPLDKLRAEIAINVHLDLTKKV 473
Qy	523	DLFGCDTQMIYDMLLKSVLPLPGDFVCKKEIGKEMYIIKHGEVQVLGGPDGPKVLV 582
Db	474	RIFADCEAGLLVELVLKLPQVSPGDIYCKKGDIGREMYIIKEGLAVV-ADGGVTQFV 532
Qy	583	TLKAGSVFGEISLLAAG---GNRRTANVVAHFANLTLTDKTLQELVHYHYPDSERILM 639
Db	533	VLDGSGYFGEISILNIGSKAGNRRRTANISIGYSDLFCLSKDOLMEALTEYEDAKTMLE 592
Qy	640	KKARVLLKQKA---KTAETATPPRKDLALLFPKKEETPKLTKLLGGTGKASLARLL--- 692
Db	593	EKGQILMKDGLDLNANAGSDPKOLEEYKVRMEGSDVLLQT-----RPARILAEY 644
Qy	693	-----KLKRFQAQK-----ENSRG-GEERG 713
Db	645	ESMQQKLQRLTKVEKPLKPLIDTFESIEGPGAESG 681
RESULT 10		
JH0560		
cyclic nucleotide-gated channel - channel catfish		
C;Species: Ictalurus punctatus (channel catfish)		
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		
C;Accession: JH0560		
R;Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Ches		
Neuron 8, 45-58, 1992		
A;Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated		
A;Reference number: JH0560; MUID:92110008; PMID:1370374		
A;Accession: JH0560		
A;Status: nucleic acid sequence not shown		
A;Molecule type: mRNA		
A;Residues: 1-682 <GOU>		
A;Cross-references: UNIPROT:P55934; GB:M83111		
A;Experimental source: olfactory epithelium		

C;Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP ar		
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-		
C;Keywords: CAMP binding; CGMP binding; ion channel; ion transport; olfacto; transmembr		
F;137-157/Domain: transmembrane #status predicted <T81>		
F;173-193/Domain: transmembrane #status predicted <T82>		
F;217-236/Domain: transmembrane #status predicted <T83>		
F;241-261/Domain: transmembrane #status predicted <T84>		
F;277-297/Domain: transmembrane #status predicted <T85>		
F;319-337/Domain: transmembrane #status predicted <T85>		
F;350-370/Domain: transmembrane #status predicted <T86>		
F;447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>		
Query Match		19.1%; Score 807.5; DB 1; Length 682;
Best Local Similarity		29.0%; Pred. No. 5.3e-42;
Matches		192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;
Qy	119	PAAPVINEYAD---AQLHNLVKRMQRORTALYKKLVEGDLSSPEA-----SPQTAKPT 168
Db	55	PSAEMLEAFTQRRPLARLVNLVLSREWA---HKSLVETE-QRPDSFLERFRGFPQAANDQ 110
Qy	169	AVPPVKESDDKPTHEYRYLLWFKVKKMPLETEYLKRIKLPNSIDSYTDRLYLWLLLVTLA 228
Db	111	SAAPA---DAPKTF-----KRWEGFVVQSDDDIYYWLFIALA 148
Qy	229	--YNNWCWFIPLRLVFPYQYQTADNIHYLLADIICDIILYDMLFIQPRLOFVRGGDIIVD 286
Db	149	SLYNW--IMLARACFDQLQDENFFLWGLDVLCDVIYILDTC-IRLRTGYLEQGLLVKD 205
Qy	287	SNELRKHYSITKFKOLDVASIIPFDICVLPFGFNPMFRANRMLKYTSFEFNHHLESIMD 346
Db	206	LAKLRDNYRTIQFKLDFLSILPTELLFFVTGVPQRFNRLLRFSRMFEFFDRTETRN 265
Qy	347	KAVYRVIRTTGYLLFILHINACVYVWASNYEGIGTRTWYDGEKNE---YLRCYVWAV 402
Db	266	YNAPFRICNLILYLVIIHWNACIYVAISKALGLSSDWTWYSGQNTLSFCYVYCYFWST 325
Qy	403	RTLITIGLPEPQTLPEIYFQLLNFPFSGVVFSSLIGOMRDVIGAATANQNYFRACMDDT 462
Db	326	LTLTTIGEMPPPVKDEYVVFVDFLVGLVIFATIVGNVGSMIANNMNAARAEFQTRIDAI 385
Qy	463	IAYMNNYSIPKLQKRVRTWYETWDSORMLDESLLKTLPTTVQLALAIQVNFISIISKV 522
Db	386	KYMHPRKNYRLETRVIKWFYLDLWTKVTDEQVILKNLDPKLRABEIAINVHLDLTKKV 445
Qy	523	DLFGCDTQMIYDMLLKSVLPLPGDFVCKKEIGKEMYIIKHGEVQVLGGPDGPKVLV 582
Db	446	RIQDCEAGLLVELVLKLPQVSPGDIYCRKGDIGKEMYIIKEGLAVV-ADGGVTQFA 504
Qy	583	TLKAGSVFGEISLLAAG---GNRRTANVVAHFANLTLTDKTLQELVHYHYPDSERILM 639
Db	505	LITAGCFGEISILNIGSKMGNNRRRTANIRSIGYSDLFCLSKDOLMEAVAEPDAQKVL 564
Qy	640	KKARVLLKQKATAEATP-----PRKDLALLFPKKEETPKLTKLLG---GT 683
Db	565	ERGRELKQGLDDESVAAGLGVIDTEKVERLDASL-----DILQTRFARLLGEFTST 619
Qy	684	GKASLARLLKXBEQA---AQKENSEGEEEG---KENEDKQKENEKQKENEKQKE 736
Db	620	QRLRKQRTALERQLCHTGLGLLSONEAGEHAGVPTHTHADIHAQPETHTRTSAETNSE 679
Qy	737	NE 738
Db	680	EE 681
RESULT 11		
S11517		
cyclic nucleotide-activated channel protein - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004		
C;Accession: S11517		
R;Dhallan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.		
Nature 347, 184-187, 1990		

A:Title: Primary structure and functional expression of a cyclic nucleotide-activated ch
A:Reference number: S11517; MUID:90370115; PMID:1697649
A:Accession: S11517
A:Molecule type: mRNA
A:Residues: 1-664 <DHA>
A:Cross-references: UNIPROT:Q00195; GB:X55519; NID:g56791; PIDN:CAA39135.1; PID:g56792
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.0%; Score 804; DB 2; Length 664;
Best Local Similarity 29.6%; Pred. No. 8.5e-42;
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;
QY 50 ESKLTKTPTVTSEEPHTNIQDKLKKSSGGTLTNPDPQNAAEPTGTVPQK---EMDP 106
DB 4 EKSNGVKSSPANN---HNHPPPSKANGKDDHRAGRPSQVAADDTSPQLRLAEMDT 60
QY 107 GKEGPNSPQKPPAAPVINEYADAQLH-----NLVKRMQRTALYKKLVEGLSSPE 159
DB 61 PRGRGGFQRIVRLVGVIRDMANKNFREEPDPSFLERF-----GPE 104
QY 160 ASPTAKPTAVPVKESDDKPTHEHYVRLVFWKVKMPLTEYLKRIKLPNSIDSYTDRLYL 219
DB 105 LQTVTHOGDDKGGKGGKGTGKKFELF-----VLDAGD-WY 143
QY 220 LMLLVTL--AYNNWCFTPLRLVPPYQADNIHWLIADIICDIILYDMLFIQRLQF 277
DB 144 RWFVIAVPVLYNW-CLLV-ARACSDLQRYVFWVLVDYFSDTVYIAD-LIIRLTGF 200
QY 278 VGGDIIIVDSNELRKHRTSTKFOLDVASIIPFDICYLFFGF-NPMFRANRLKYSFPE 336
DB 201 LEQGLLVKDPKRLRNYHTLOFKLDVASIITDLYPAVGTHSPVFRNLLHPARFPE 260
QY 337 FNHLESIMDKAYIRVIRTTCYLLFILHINACVYVWASNYEGIGTTRWY----DGE-- 390
DB 261 FPDRTETSTPNIRISNLVLIIVIIHNACIYIVYSKSIIGFGVDTWVYVNPITDPY 320
QY 391 --GNEYLCRYWAVRTLTITIGLPEPQTLFEIVFOLLNFFSGVFVSSLIIGOMRDVIGAA 448
DB 321 VLAREYIYCLYWSLTLTITIGETPPVXDDEVLVFIQDLGLVIFATIVGNVSGMISNM 380
QY 449 TANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMDESDLLKTLPTVOL 508
DB 381 NATRAEFOAKIDAVHYMQFRKVSXDMKAVIKWPDYLTNKTVDREVLKLPKALRA 440
QY 509 ALAIDVNSIISKVDLFKGCOTMIYDMLRLKSVLYLPGDPVCKKGIGKEMYYIKKE 568
DB 441 EIAINVHLSLTKKVRIFODCEAGLLVELVLKLPQVFSQDYICRKGDIGKEMYYIKKEG 500
QY 569 VQVLGGPDGTVLVTLKAGSFGFISLLAAG--GNRRRTANVAHGFANLLTLDDKTLQ 625
DB 501 LAVV-ADGVVTQYALLSAGSCEGEISILNIGSKWGNRTANIRSLGSDILFCLSKDLM 559
QY 626 EILVHYPSERILMKKARVLLKQAKTAE---ATPPRKDLALLPPKBEETPKLFKTLGG 682
DB 560 BAVTEYDPAKKVLEBGRGAILMKEGLLDENEVAASMEVDV-----QSKLEQLETNM--D 611
QY 683 TGKASLARKLLKREQAQKKNSEGGEGEKENEDKQEN--EDKQKENEDKGENEDX 740
DB 612 TLYTRFARLL-----ABYTGAAQQLKORITVLETKMQNH-----EDDYL 651
QY 741 DKGREPEKPLDRPCTAS 759
DB 652 SDG-----INTPEPTAA 663

RESULT 12

JC6509

rod cyclic nucleotide-gated cation channel protein alpha-chain - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C:Accession: JC6509

R.Veske, A.; Nilsson, S.E.G.; Gal, A.

Gene 202, 115-119, 1997

A:Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-subunit
A:Reference number: JC6509; MUID:98087425; PMID:9427553

A:Accession: JC6509

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-691 <VES>

A:Cross-references: UNIPROT:Q28279; EMBL:X99914; NID:g1488571; PIDN:CAA68186.1; PID:g1488571
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
F:478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 18.9%; Score 801.5; DB 2; Length 691;
Best Local Similarity 29.2%; Pred. No. 1.3e-41;
Matches 220; Conservative 136; Mismatches 286; Indels 112; Gaps 23;
QY 21 EQSRREEGSHPSNQSOQTAAQENKGEESLTKTSPVTSEEPHTNIQDKLKKNSG 80
DB 24 EKEIRRMENGARSS-----FSDDDDDDSDSASMFEE---ENETPHA--RDSCRNSQRR 72
QY 81 DLTTNPDPQNAAEPTGTVPQKEMDPGKEGPNSPQKPPAAPVINEYADAQLHNLVKRMR 140
DB 73 D-----PSQRE-----QYLPGAIALFNVNSSNKEQEPKKEK 104
QY 141 QRTALYKKLVEGLSSPEASPTAKPTAVPVKESDDKPTHEHYVRLVFWKVKMPLTEY 200
DB 105 KKKK--EKKSXSGDKNENKDKSEKKKKE---KEKEKKNKEK-----GKDKK---EEE 150
QY 201 LKRIKLPNSIDSYTDRLVLLMLLVTL--AYNNWCFTPLRLVPPYQADNIHWLIADI 258
DB 151 KKEVMV---IDP-AGNMYYNLFCITLPMVYNT--MVIAACDFDELQSDYLEWYIIFDY 204
QY 259 ICDIILYDMLFIQRLQFVRGGDIIIVDSNELRKHRTSTKFOLDVASIIPFDICYLFFG 318
DB 205 LSDIVLLDM-FVTRTGYLEQGLLVREAKLIEKYSKLNQFKDLFSLVITDILLYFKLG 263
QY 319 FN-PMFRANRLKYSFPEFNHLESIMDKAYIRVIRTTCYLLFILHINACVYVWASNY 377
DB 264 WNYFEIRLNRLRISRMFEFPQRTETRTNYPNIRISNLVMIYVIIHNACVYFSIKA 323
QY 378 EGIGTTRWY----DGE-----GNEYLCRYWAVRTLTITIGLPEPQTLFEIVFOLLNFFS 429
DB 324 IGFNGDWTWVYDVNDPEFGRLLARKYVSYLSYWSLTLTITIGETPPVRDSEYVFWVDL 383
QY 430 GVVFSSLIIGOMRDVIGAAATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDS 489
DB 384 GVLFIATIVGNISNMNAARAEFQARIDAIQYWHFRNVSKDMKRVIKWFDYLTWN 443
QY 490 QRMLEDSDLLKTLPTVOLALADVNFSSIISKVDLFKGCOTMIYDMLRLKSVLYLPGD 549
DB 444 KKTVDKEVLKYLFDKLRAEIATINVHLDTLKKVRIFADCEAGLLVELVLKLPQVYSPGD 503
QY 550 FVCKKGIGKEMYYIKKEGVOLGGPDGTVLVTLKAGSFGFISLLAAG--GNRRRTA 606
DB 504 YICKKGIGKEMYYIKKEGLAVV-ADDGITQFVVLSDGSYFGEISILNIGSKAGNRRTA 562
QY 607 NVVAHGFANLLTLDDKTLQETLVHYPSERILMKKARVLLKQAKTAE---KTEATPPRKDL 662
DB 563 NIKSIGISDILFCLSKDLMLEALTEYDPAKTLMBEKGQILMKOGLDININAGSDPKDL 622
QY 663 ALLFPKBEETPKLFKTLGGTGKASLARLLKLRQAQKKNSEGGEGEKENEDKQKE 722
DB 623 EEKVTREMGSDVLLAQT-----RFARIL-----AYESMQOK 653
QY 723 NEDKQKENEDKGENEDK-----KGREPEEKPLD 752
DB 654 LKQRLTKVERFLKPIIDTFSALEGTGDSRPLD 687

RESULT 13

S07103

cGMP-gated ion channel protein - bovine

C:Species: Bos primigenius taurus (cattle)


```

Db      548 VV-AEDGTFQVVLGDGSGYFGEISILNITKSGKGNRRNTANIRSGISDLFCLSKDDLMEA 606
Qy      628 LVHYDPSERILMKAR-VLLQKQ---AKTAETPPKDLALILFPKKEETPKLFKTLGGT 683
Db      607 LTEXPEAKKALEKGRQILMKNDLIDEELAKAGADPKDI-----EEKVEHLETSLSL 659
Qy      684 GKASLARLL-----KLKREQQAQKEN 705
Db      660 -QTFARLLAEYNATQMKVKORLSQLES 686

RESULT 15
150680
alpha subunit of rod photoreceptor CNG-channel - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50680
R:Bonigk, W.; Altenhofen, W.; Muller, F.; Does, A.; Illing, M.; Molday, R.S.; Kaupp, U.B
Neuron 10, 865-877, 1993
A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A:Reference number: I50630; MUID:93264082; PMID:7684234
A:Accession: I50680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-645 <BON>
A:Cross-references: UNIPROT:Q09080; EMBL:X89599; NID:G908852; PIDN:CAA61758.1; PID:G9088
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match      18.2%; Score 771; DB 2; Length 645;
Best Local Similarity 34.3%; Pred. No. 8.7e-40;
Matches 173; Conservative 104; Mismatches 196; Indels 32; Gaps 12;

Qy      217 LVLLWLLLVTL--AYNWCWFIPLRVPYQYADNIHWLIADIICDIIILYDMLFIQPR 274
Db      116 MYNWLFCITWPMVNWNT--MIARACDFEQLNDYLAWFIVDVSDVIYIADM-FVETR 172
Qy      275 LQFVRGGDIIIVDSNELRKHRTSTKFDLDAVASIIPFDICYLFFGFN-PMFRANRMLKYTS 333
Db      173 TGYLEQGLLVKEEQKLEKYKSSLQKDLFLSIPTDLLYFKLGLNYPELRINLLRVAR 232
Qy      334 FFEFNHLESIMDKAYIVRVIRTTGYLLFILHNACVYWNASNYEGIGTTRWVYDGEQN- 392
Db      233 MFEFFQRTETRTNYPENFRISNLVMIYIIHWNACVYYSISKAIGFGADTWVYPTNSHP 292
Qy      393 -----EYLACYWYAVTLITIGLPEPQTLFEIVFOLLNFFSGVFVFSLLIGMRDVI 445
Db      293 EFARLTRKYVSLYVSTLTITIGTPPPVRDSEYFFVVVDPLVGLVLPATIVGVGSMI 352
Qy      446 GAATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMDELSDLLKLTPTT 505
Db      353 SNMNAARAEFAQIDAIKQYMHFRNVSKMEKVKWFDYLTWNKKAVDREVLKYLDPDK 412
Qy      506 VOLALAIQVNFISIISKVDFKCDQTMIDMLRLKSVLYLPQDFVCKKGIGKEMYYIK 565
Db      413 LRAETAINVHLETLKKRIFADCEAGLLVELVLQPOVSPGVYICRKGDIGREMYIIK 472
Qy      566 HGEVQVLGGPDGTVLVTLKAGSVGEISLLAAG--GNERTANVAHGFANLLTLDDK 622
Db      473 EGKLAW--ADGVTQFVVLSDGSYFGEISILNITKSGKGNRRNTANIRSGISDLFCLSKD 531
Qy      623 TLQELVHYDPSERILMKAR-VLLKQKAKTAETPPPKDLALLFPKKEETPKLFKTLGG 681
Db      532 DLMEALTEYPAKAMLEKKGQILMKDGLLDIEVANLGSD-----PKOLEKV--AYME 583
Qy      682 GTG---KASLARLLKLKREQQAQKK 703
Db      584 GMDRLQTKFARL--LAEYDAQAQK 606
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 27, 2005, 18:08:36 ; Search time 130 Seconds
(without alignments)
3186.708 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234

Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSAEGGEVLTVKKEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	1 CNB3 HUMAN	Q9ngw8 homo sapien
2	3181.5	75.1	782	1 CNB3 CANFA	Q8mjld canis famil
3	2515	59.4	694	1 CNB3 MOUSE	Q9ijz9 m cyclic-nu
4	1971.5	46.6	866	2 Q80X18	Q80x18 mus musculu
5	1959	46.3	1339	2 Q35788	Q35788 rattus norv
6	1952	46.1	1245	2 Q43636	Q43636 homo sapien
7	1949	46.0	909	1 CNB4 HUMAN	Q14028 homo sapien
8	1949	46.0	1251	2 Q9UMG2	Q9umg2 homo sapien
9	1923	45.4	858	2 Q55157	Q55157 rattus norv
10	1920	45.3	938	2 Q77658	Q77658 bos taurus
11	1920	45.3	948	2 Q77659	Q77659 bos taurus
12	1920	45.3	952	2 Q77660	Q77660 bos taurus
13	1920	45.3	1394	1 CNB4 BOVIN	Q28181 bos taurus
14	1103	26.1	1040	2 Q9W2D5	Q9w2d5 drosophila
15	1096	25.9	800	2 Q90975	Q90975 caenorhabdi
16	1095	25.9	800	2 Q62237	Q62237 caenorhabdi
17	878	20.7	515	2 Q9S5L0	Q9s5l0 drosophila
18	850	20.1	694	1 CNB3 HUMAN	Q16281 homo sapien
19	831.5	19.6	683	1 CNB3 RAT	Q62927 r cgm-gate
20	829	19.6	663	1 CNB2 BOVIN	Q30341 bos taurus
21	826.5	19.5	698	2 Q6ZNA7	Q6zna7 homo sapien
22	823.5	19.4	684	1 CNB1 MOUSE	Q29974 m cgm-gate
23	821.5	19.4	735	1 CNB1 CHICK	Q90805 gallus gall
24	818.5	19.3	664	1 CNB2 RABIT	Q28718 oryctolagus
25	818	19.3	686	2 Q9N0H4	Q9n0h4 sus scrofa
26	817	19.3	686	1 CNB1 HUMAN	P29973 h cgm-gate
27	807.5	19.1	682	1 CNB1 ICTPU	P55934 ictalurus p
28	806	19.0	611	2 Q9QWV7	Q9qwn7 rattus norv
29	806	19.0	632	2 Q9ER32	Q9er32 rattus norv
30	806	19.0	670	2 Q9ER33	Q9er33 rattus norv
31	804	19.0	664	1 CNB2 RAT	Q00195 rattus norv

32	801.5	18.9	691	1	CNB1 CANFA	Q28279 c cgm-gate
33	797	18.8	690	1	CNB1 BOVIN	Q00194 b cgm-gate
34	794	18.8	706	1	CNB3 BOVIN	Q29441 bos taurus
35	789.5	18.6	664	2	Q80X18	Q80x18 mus musculu
36	788.5	18.6	631	1	CNB3 MOUSE	Q9ijz8 mus musculu
37	788.5	18.6	631	2	Q8CFV6	Q8cfv6 mus musculu
38	788.5	18.6	733	1	CNB3 CABEL	Q03611 caenorhabdi
39	787.5	18.6	1218	2	Q9W201	Q9w201 drosophila
40	783.5	18.5	637	2	Q80416	Q80416 carassius a
41	777.5	18.4	664	1	CNB2 MOUSE	Q62398 mus musculu
42	771	18.2	645	1	CNB3 CHICK	Q90980 gallus gall
43	768.5	18.2	799	2	Q7PTE6	Q7pte6 anopheles g
44	759	17.9	1453	2	Q8IR35	Q8ir35 drosophila
45	759	17.9	1463	2	Q9U5E2	Q9u5e2 drosophila

ALIGNMENTS

RESULT 1
CNB3 HUMAN
ID CNB3 HUMAN STANDARD; PRT; 809 AA.
AC Q9NQW8; Q9NRE9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
DE (Cyclic nucleotide gated channel beta 3) (Cone photoreceptor cGMP-gated channel beta subunit) (Cyclic nucleotide-gated cation channel modulatory subunit).
GN Name=CNGB3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, VARIANT ACHM3 PHE-435, AND VARIANTS PRO-298 AND GLY-755.
RX MEDLINE=20414632; PubMed=10958649; DOI=10.1093/hmg/9.14.2107;
RA Kohl S., Baumann B., Broghammer M., Jaegle H., Sieving P., Kellner U., Spegal R., Anastasi M., Zrenner E., Sharpe L.T., Missinger B.;
RT "Mutations in the CNGB3 gene encoding the beta-subunit of the cone photoreceptor cGMP-gated channel are responsible for achromatopsia (ACHM3) linked to chromosome 8Q21.";
Hum. Mol. Genet. 9:2107-2116(2000).
[2]
RP SEQUENCE OF 114-809 FROM N.A. (ISOFORM 2), FUNCTION, SUBUNIT, VARIANT ACHM3 PHE-435, AND VARIANT CYS-234.
RC TISSUE=Retina;
RX MEDLINE=20347712; PubMed=10888875; DOI=10.1038/77162;
RA Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.N., Silva E.D., Maunee I.H.;
RT "Genetic basis of total colourblindness among the Pingelapese islanders.";
Nat. Genet. 25:289-293(2000).
-1- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod photoreceptors. Induced a flickering channel gating, weakened the outward rectification in the presence of extracellular calcium, increased sensitivity for L-cis diltiazem and enhanced the cAMP efficiency of the channel when coexpressed with CNGA3 (by similarity). Essential for the generation of light-evoked electrical responses in the red-, green- and blue sensitive cones.
-1- SUBUNIT: Heterooligomeric complex with CNGB3.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=Q9NQW8-1; Sequence=Displayed;
Name=2;
IsoId=Q9NQW8-2; Sequence=VSP_009742;

Note=No experimental confirmation available;
 -i- TISSUE SPECIFICITY: Expressed specifically in the retina.
 -i- DISEASE: Defects in CNGB3 are a cause of achromatopsia 3 (ACHM3) [MIM:262300]; also known as Pingelapese blindness. ACHM3 is a congenital complete achromatopsia and is distinct from total colorblindness mainly because of the consistent concurrence of severe myopia.
 -i- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
 -i- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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 EMBL; AF272900; AAF86274.1; -;
 EMBL; AF228520; AAF80179.1; ALT_INIT.
 Genew; HGNC:2153; CNGB3.
 MIM; 262300; -;
 InterPro; IPR000595; cNMP binding.
 InterPro; IPR005821; Ion Trans.
 InterPro; IPR001622; K-channel_pore.
 Pfam; PF00027; cNMP_binding; 1.
 Pfam; PF00520; Ion_trans; 1.
 SMART; SM00100; cNMP; 1.
 PROSITE; PS00889; CNMP_BINDING_1; 1.
 PROSITE; PS00888; CNMP_BINDING_2; 1.
 PROSITE; PS00442; CNMP_BINDING_3; 1.
 KW Alternative splicing; cGMP-binding; Disease mutation; Ion transport; Ionic channel; Multigene family; Polymorphism; Transmembrane; Vision.
 FT DOMAIN 1 216
 TRANSMEM 217 237
 DOMAIN 238 250
 TRANSMEM 251 271
 DOMAIN 272 302
 TRANSMEM 303 323
 DOMAIN 324 359
 TRANSMEM 360 380
 DOMAIN 381 417
 TRANSMEM 418 438
 DOMAIN 439 504
 TRANSMEM 505 525
 DOMAIN 526 809
 NP_BIND 532 676
 BINDING 592 592
 BINDING 604 604
 CARBOHYD 468 468
 VARSPLIC 590 594
 VARIANT 234 234
 VARIANT 298 298
 VARIANT 435 435
 VARIANT 755 755
 SEQUENCE 809 AA; 92249 MW; AC23B7072C1C7DB3 CRC64;
 Query Match 100.0%; Score 4234; DB 1; Length 809;
 Best Local Similarity 100.0%; Pred. No. 1.3e-229;
 Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPKSLTKVNVKVPKIGENNEQSSRRNEGSHPSNOSQOQTAEKNGREKSLTKKSTPV 60
 DB 1 MPKSLTKVNVKVPKIGENNEQSSRRNEGSHPSNOSQOQTAEKNGREKSLTKKSTPV 60
 QY 61 TSEBPHNTIQDKLSKKNSSGDLTTNPDQNAEPTGTVPQKEMDPGKGPNSPQNKPPA 120

DB 61 TSEBPHNTIQDKLSKKNSSGDLTTNPDQNAEPTGTVPQKEMDPGKGPNSPQNKPPA 120
 QY 121 AVINEYADAQAHNLVKRMROQTALYKKLVGDLSSPEASPTAKPTAVPPVKESDDKP 180
 DB 121 AVINEYADAQAHNLVKRMROQTALYKKLVGDLSSPEASPTAKPTAVPPVKESDDKP 180
 QY 181 TBHYRLRLWFKVKMPLTEYLKRIKLPSIDSYTDRLYLWLLVTLAYNNWCWFLPLRL 240
 DB 181 TBHYRLRLWFKVKMPLTEYLKRIKLPSIDSYTDRLYLWLLVTLAYNNWCWFLPLRL 240
 QY 241 VFPYQADNIHWLIADIICDIIYIDMLFIQPRQLQFVRGGDIIVDSELNKHRTSTKF 300
 DB 241 VFPYQADNIHWLIADIICDIIYIDMLFIQPRQLQFVRGGDIIVDSELNKHRTSTKF 300
 QY 301 QLDVASIIPFDICYLFFGNPMFRANMLKYTSFEFNHLESIMDKAYIVIRITGVL 360
 DB 301 QLDVASIIPFDICYLFFGNPMFRANMLKYTSFEFNHLESIMDKAYIVIRITGVL 360
 QY 361 LFIILINACVYVWASNYEGITTRWYDGEQNEYLRCYYWAVRTLITIGLPEPQTLFEI 420
 DB 361 LFIILINACVYVWASNYEGITTRWYDGEQNEYLRCYYWAVRTLITIGLPEPQTLFEI 420
 QY 421 VFQLLNFFSGVFVSSLIQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKLQKRV 480
 DB 421 VFQLLNFFSGVFVSSLIQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKLQKRV 480
 QY 481 TWYEYTWDSQRMLESLLKTLPTVOLALADVNFISISKVDLPKGCOTMIYDMLRL 540
 DB 481 TWYEYTWDSQRMLESLLKTLPTVOLALADVNFISISKVDLPKGCOTMIYDMLRL 540
 QY 541 KSVLYLPDGFVCKKGEGIKEMWIIKHGEVQVGLGGPDGTVLTKAGSVFGESLAAAG 600
 DB 541 KSVLYLPDGFVCKKGEGIKEMWIIKHGEVQVGLGGPDGTVLTKAGSVFGESLAAAG 600
 QY 601 GNRRTANVVAHGFANLLTLDKKTLQEIILVHYVDPDSERILMKKARVLLKQAKTAEATPPRK 660
 DB 601 GNRRTANVVAHGFANLLTLDKKTLQEIILVHYVDPDSERILMKKARVLLKQAKTAEATPPRK 660
 QY 661 DLALLFPPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEEGKEDKQ 720
 DB 661 DLALLFPPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEEGKEDKQ 720
 QY 721 KENEDKQKENEKQKENEKDKGRPEEKPLDRPECTASPIAVEEPHVSRRITVLPRTS 780
 DB 721 KENEDKQKENEKQKENEKDKGRPEEKPLDRPECTASPIAVEEPHVSRRITVLPRTS 780
 QY 781 RQSLIISMAPSAGGEEVLTIIEVKKAKQ 809
 DB 781 RQSLIISMAPSAGGEEVLTIIEVKKAKQ 809
 RESULT 2
 CNB3_CANFA STANDARD; PRT; 782 AA.
 ID CNB3_CANFA
 AC Q8MJU7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
 DE (Cyclic nucleotide-gated channel beta 3) (Cone photoreceptor cGMP-gated channel beta subunit) (Cyclic nucleotide-gated cation channel modulatory subunit).
 GN Name=CNGB3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT CD ASN-262.
 RX PubMed=12140185; DOI=10.1093/hmg/11.16.1823;
 RA Sidjanin D.J., Lowe J.K., McElwee J.L., Milne B.S., Phippen T.M., Sargan D.R., Aguirre G.D., Acland G.M., Ostrander E.A.;

RT "Canine CNGB3 mutations establish cone degeneration as orthologous to
 RL the human achromatopsia locus ACHM3.";

CC Hum. Mol. Genet. 11:1823-1833(2002).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cGMP which leads to an opening of the cation

CC channel and thereby causing a depolarization of rod
 CC photoreceptors. Induced a flickering channel gating, weakened the
 CC outward rectification in the presence of extracellular calcium,
 CC increased sensitivity for L-cis diltiazem and enhanced the cAMP
 CC efficacy of the channel when coexpressed with CNGB3. Essential for
 CC the generation of light-evoked electrical responses in the red,
 CC green- and blue sensitive cones (By similarity).

CC -!- SUBUNIT: Heterooligomeric complex with CNGB3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- DISEASE: Defects in CNGB3 are a cause of cone degeneration (cd).
 CC Cd is characterized by day-blindness and absence of retinal cone
 CC function. This autosomal recessive disorder occurs naturally in
 CC the Alaskan Malamute and German Shorthaired Pointer breeds.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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DR EMBL; AF490511; AAM89224.1; -
 DR InterPro; IPR000595; CNMP_binding.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K_channel_pore.

DR Pfam; PF00027; CNMP_binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.

DR SMART; SM00100; CNMP; 1.

DR PROSITE; PS00888; CNMP_BINDING_1; 1.

DR PROSITE; PS00889; CNMP_BINDING_2; 1.

DR PROSITE; PS00042; CNMP_BINDING_3; 1.

KW cGMP-binding; Disease mutation; Ion transport; Ionic channel;

Multigene family; Transmembrane; Vision.

FT DOMAIN 1 211 Cytoplasmic (Potential).

FT TRANSMEM 212 232 H1 (Potential).

FT DOMAIN 233 245 Extracellular (Potential).

FT TRANSMEM 246 266 H2 (Potential).

FT DOMAIN 267 297 Cytoplasmic (Potential).

FT TRANSMEM 298 318 H3 (Potential).

FT DOMAIN 319 412 Extracellular (Potential).

FT TRANSMEM 413 433 H4 (Potential).

FT DOMAIN 434 493 Cytoplasmic (Potential).

FT TRANSMEM 494 514 H5 (Potential).

FT DOMAIN 515 572 Extracellular (Potential).

FT TRANSMEM 573 593 H6 (Potential).

FT DOMAIN 594 782 Cytoplasmic (Potential).

FT NP_BIND 527 671 cGMP (By similarity).

FT BINDING 587 587 cGMP (By similarity).

FT BINDING 599 599 cGMP (By similarity).

FT VARIANT 262 262 D -> N (in cd; in a German Shorthaired Pointer).

SEQUENCE 782 AA; 89424 MW; 7139EF3B86268A79 CRC64;

Query Match 75.1%; Score 3181.5; DB 1; Length 782;

Best Local Similarity 76.2%; Pred. No. 1.8e-170;

Matches 618; Conservative 57; Mismatches 105; Indels 31; Gaps 5;

Oy 1 MFSLT-KVNVKPIGENNEQSRNEEGSPNSQSQQTAAQENKGEKSLTKSTP 59

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MFSLTIKSNKVKPRENDENKQD-----PDPSNQFQSQTRQGENSKSLQTKWTP 53

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 60 VTSEPHNTN1QDKLSKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKGNPSQNKPP 119

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 54 VTFEESHAKMOKDKISEKNLSRLDLTTNPNHQHTPTSEKMSQKEMETKGEGLVSPKSKPL 113

Oy 120 AAPVINEYADAQLHNLVKRMQRQTALYKKKLVEGLDSSPEASPTAKPTAPVPPVKESDDK 179

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 114 GVPVINEYADAQLHNLVKRMQRQTALYKKKLVEGLDSSPEASPTAKPTAPVSPQESNAK 173

Oy 180 -PTHYRLLWFKVKKMPLTEYLKRIKPNISIDYTDRLYLLWLLVTLAYNWCWFLPL 238

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 174 LKEEYHYTHILCFKQKMPLEKYLKRFRLPGSIDYTDRLYLLWLLVTLAYNWCWFLPL 233

Oy 239 RLVPYPTADNIHWLADIIICDIYLYDMLFOPRLQFVRRGGDIIVDSNELRKHRTST 298

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 234 RLVPYPTADNIHWLADIIICDIYLYDMLFOPRLQFVRRGGDIIVDSNELRKHRTST 293

Oy 299 KFQLDVASIIPFDICYLFFGFNPMFRANMLKYTSFFEFNHLESIMDKAYIYVIRTTG 358

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 294 KFQLDVASIIPFDICYLFFGFNPMFRANMLKYTSFFEFNHLESIMDKAYIYVIRTTG 353

Oy 359 YLLFILHINACVYTWASNYRGIGTRWYDGGNEYLRCYVAVRTLTITIGLPEPQTLF 418

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 354 YLLYTLHINACVYTWASNYRGIGTRWYDGGNEYLRCYVAVRTLTITIGLPEPQTLF 413

Oy 419 EIVFQLNFFSGVFVFSLLIGOMEDVIGAATANONYFRACMDDTIAYMNNYSIPKLQKR 478

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 414 EIVFQLNFFSGVFVFSLLIGOMEDVIGAATANONYFRACMDDTIAYMNNYSIPKLQKR 473

Oy 479 VRTWYETWDSQRMLESDDLKTLPTVQLALADVNFISIISKVDLFKGCQTQMIYDMLL 538

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 474 VRTWYETWDSQRMLESDDLKTLPTVQLALADVNFISIISKVDLFKGCQTQMIYDMLL 533

Oy 539 RLKSVLYLPGDFVCKGKEIGKEMYYIKHGEVQVVGDPGDKVLVTLKAGSVFGESILAA 598

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 534 RLKSVLYLPGDFVCKGKEIGKEMYYIKHGEVQVVGDPGDKVLVTLKAGSVFGESILAA 593

Oy 599 GGNRRRTANVAHGFANLLTLDKKTQELIIVHYVDPSEKILMKKARVLLKQAKATAETPP 658

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 594 GGNRRRTANVAHGFANLLTLDKKTQELIIVHYVDPSEKILMKKARVLLKQAKATAETPP 653

Oy 659 RKDLALLFPKKEETPKLTKLGGTGKASLARLLKREQAQKKNSEGESEEGKENED 718

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 654 RKGLAFLFPKKEETPKLTKLGGTGKASLARLLKREQAQKKNSEGESEEGKENED 706

Oy 719 KQENEDKQENEDKQENEDKQREPEKPLDRPCTASPIAVEEPHSVRVTLVPRG 778

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 707 -----GKRREVEDKEREPESEKILDSSECRANCIITAEEMPQSIIRRAALPRG 751

Oy 779 TSROSLIISMAPSAEGGEVLTIEVKEKAKQ 809

Db 752 TTROSLIISMAPSAEGGEVLTIEVKEKAKQ 782

RESULT 3

CNGB3_MOUSE
 ID CNB3_MOUSE STANDARD; PRT; 694 AA.
 AC Q9JZ9;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
 DE (Cyclic nucleotide-gated channel beta 3) (Cone photoreceptor cGMP-
 DE gated channel beta subunit) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit) (Cyclic nucleotide-gated channel .subunit CNGB6).
 GN Name=Cngb3; Synonym=Cng6;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A. FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 RX MEDLINE=20130348; PubMed=10662822;
 RA Gerstner A., Zong X., Hofmann F., Biel M.;
 RT "Molecular cloning and functional characterization of a new modulatory

RT cyclic nucleotide-gated channel subunit from mouse retina.";

RL J. Neurosci. 20:1324-1332(2000).

CC -|- FUNCTION: Visual signal transduction is mediated by a G-protein

CC coupled cascade using cGMP as second messenger. This protein can

CC be activated by cGMP which leads to an opening of the cation

CC channel and thereby causing a depolarization of rod

CC photoreceptors. Essential for the generation of light-evoked

CC electrical responses in the red-, green- and blue sensitive cones

CC (by similarity). Induced a flickering channel gating, weakened the

CC outward rectification in the presence of extracellular calcium,

CC increased sensitivity for L-cis diliazem and enhanced the cAMP

CC efficacy of the channel when coexpressed with CNGB3.

CC -|- SUBUNIT: Heterooligomeric complex with CNGB3.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- TISSUE SPECIFICITY: Small subset of retinal photoreceptor cells and

CC testis.

CC -|- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel

CC (TC 1.A.1.5) family.

CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC -----

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CC -----

DR EMBL; AJ243572; CAB71152.1; -.

DR MGD; MGI:1353562; CnGB3.

DR GO; GO:0005886; C:plasma membrane; IC.

DR GO; GO:0030553; F:3', 5'-cGMP binding; IC.

DR GO; GO:0005223; F:intracellular cGMP activated cation channel. . .; IPI.

DR GO; GO:0009187; P:cyclic nucleotide metabolism; IC.

DR InterPro; IPR005095; cNMP binding.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K+channel_pore.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; Ion trans; 1.

DR SMART; SM00100; cNMP; 1.

DR PROSITE; PS00888; cNMP BINDING_1; 1.

DR PROSITE; PS00889; cNMP BINDING_2; 1.

DR PROSITE; PS50042; cNMP BINDING_3; 1.

KW cGMP-binding; Ion transport; Ionic channel; Multigene family;

KW Transmembrane; Vision.

FT DOMAIN 1 209 Cytoplasmic (Potential).

FT TRANSMEM 210 230 H1 (Potential).

FT DOMAIN 231 242 Extracellular (Potential).

FT TRANSMEM 243 263 H2 (Potential).

FT DOMAIN 264 294 Cytoplasmic (Potential).

FT TRANSMEM 295 315 H3 (Potential).

FT DOMAIN 316 351 Extracellular (Potential).

FT TRANSMEM 352 372 H4 (Potential).

FT DOMAIN 373 409 Cytoplasmic (Potential).

FT TRANSMEM 410 430 H5 (Potential).

FT DOMAIN 431 568 Extracellular (Potential).

FT TRANSMEM 569 589 H6 (Potential).

FT DOMAIN 590 694 cGMP (By similarity).

FT NP_BIND 524 668 cGMP (By similarity).

FT BINDING 584 584 cGMP (By similarity).

FT BINDING 596 596 cGMP (By similarity).

FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 694 AA; 79722 MW; 0B9F9CF3B180DA82 CRC64;

Query Match 59.4%; Score 2515; DB 1; Length 694;

Best Local Similarity 68.7%; Pred. No. 4.4e-133;

Matches 485; Conservative 92; Mismatches 113; Indels 16; Gaps 7;

Qy 1 MFKSLT-KVNVKPIGNNENEGSRNREGSPH--SNOSQQTAAQENKGEKSLTKTS 57

Db 1 MLKSLTKVFNKNVPM-----EGRMKKLCNLISSSQPTAAGDQKQEPURSR- 50

Qy 58 TPVTSEPHNTNIQDLKSKKNSGDLTTNPDQNAABPTGTVPROKEMDFGKGNPSPQNK 117

Db 51 TPITFEKSHK-EDNSTGNSLRDFTPNPDPECRABLTTRTMAEMKTRGKRPVSFKTK 109

Qy 118 PPAAPVINEYADAQLHNLVKRMORTALYKKKLVGSD-LSSPEASQTAKPATVPPVKES 176

Db 110 VLETSIINEYTAHLHNLVEMRERTALYKKTLTBEENFEVEASQTAAMSTNISPKQEN 169

Qy 177 DKPTEHYVRLWFKVKMPLTEYLKRIKLPNSIDSYDRLVLLMLLLVTLAYNNCWFI 236

Db 170 NSKLKEH-QDTSEFKQRPVVEHLRMLPRLPSIDSYDRLVLLMLLLVTLAYNNCWLL 228

Qy 237 PLRLVFPYQYADNIHYWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHRT 296

Db 229 PVRLVFPYQYADNIHYWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHRT 288

Qy 297 STKFQDLVASIIPDFICYLFGFNPMFRANRMLKYSFPEFNHLESIMDKAYIRVIRT 356

Db 289 STKFRMDVASLPEFLYIFFGVNPFRANRMLKYSFPEFNHLESIMDKAYIRVIRT 348

Qy 357 TGYLLFILHINACVYVWASNYEGIGTRVWYDGEYVYVWVAVRTLTITIGGLPEPOT 416

Db 349 TGYLLFILHINACVYVWASNYEGIGTRVWYDGEYVYVWVAVRTLTITIGGLPEPOT 408

Qy 417 LFEIVFQLNPFSGVVFSSLLIGQMRDVIQATANQNYFRACMDPTIAYNNYSIPKLYQ 476

Db 409 SFEIVFQLNPFSGVVFSSLLIGQMRDVIQATANQNYFRACMDPTIAYNNYSIPKLYQ 468

Qy 477 KVRVWYETWDSQRMDESLLKTLPTVLOALADVNFSISKVDLEKGCOTQMIYDM 536

Db 469 YRVRTWLEYTWSQRLDESLLKTLPTVLOALADVNFSISKVDLEKGCOTQMIYDL 528

Qy 537 LLRLKSLVLPDGFVCKKGEIKEMVYIKHGVQVLGGDGTGKVLVTLKAGSVFGEISLL 596

Db 529 LLRLKSLVLPDGFVCKKGEIKEMVYIKHGVQVLGGDGTGKVLVTLKAGSVFGEISLL 588

Qy 597 AAGGGRRTANVVAHGAFANLLTDLKKTQLLEIIVHYVPSRILMKKARVLLKQAKTAET 656

Db 589 AAGGGRRTANVVAHGAFANLLTDLKKTQLLEIIVHYVPSRILMKKARVLLKQAKTAET 648

Qy 657 PPRKDLALLFPKKEETPKLFTLLGGTGKASLARILLKLRQAAQK 702

Db 649 PARPGAPLFPKKEETPKLFTLLGGTGKASLARILLKLRQAAQK 694

RESULT 4

Q80XL8 PRELIMINARY; PRT; 866 AA.

ID Q80XL8

AC Q80XL8

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE CnGB1b protein (Fragment).

GN Name=CnGB1b;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Eye;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny R.A., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

QY	515	NSFSIIKVDL	FKGCDTQMIYDMLRLRLKSVLYLPGDFVCKKGEIGKEMYLIIKHGEVQVLGG	574
Db				
Db	570	NYSIVSKVAL	FOGCDRQMFIMDLKRLRSVYLPNDYVCKKGEIGREMYIIIQAGQVQVLGG	629
QY	575	PDGTKVLT	LTKAGSVGEISLLAAGGNGRTANVVAHGFANLTLDKKTKLOEILLVHYVPS	634
Db				
Db	630	PDGKAVLT	LTKAGSVGEISLLAAGGNGRTANVVAHGFNLFLDKDLNEILLVHYVES	689
QY	635	ERILMKARV	LLKQAKTAETAPPRKDLALLFPFKBETPKLFKTLTLLGGTGKAS	687
Db				
Db	690	QKLLRKARR	MLRNNNK----PKEEKSVLLFPFRAGTPKLFNAALAAAGKMGPRGAKGG	744
QY	688	-----	LARLLKLRBOAA-----OKNENSGGEEBEGKENEDKQKENEDKQKENEDKXG	734
Db				
Db	745	KLHLRLRL	KELTAALAEAAARQQQLLBQAKSSQBAGGEGSGATDQAPAPQEP	795
QY	735	KENEDKGR	EPKEPLDRPECTASPIAVEEBPHSVRRTVLPRTGTSRQSLIISMAPSAEG	794
Db				
Db	796	PPKDPK	PPGPPE-----PSAQSSPPASAKPE--ESTGEAAGPPPEPSVIRVSPGDP	848
QY	795	GEEVLTV	IEVKEKAKQ 809	
Db				
Db	849	GEQTL	SVLEVLEKKE 863	
RESULT 5				
O35788				
ID	O35788	PRELIMINARY;	PRT; 1339 AA.	
AC	O35788;			
DT	01-JAN-1998	(TrEMBLrel. 05, Created)		
DT	01-JAN-1998	(TrEMBLrel. 05, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Cyclic nucleotide-gated channel beta subunit.			
GN	Name=CNG4.1;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RC	Sauter A., Biet M., Hofmann F.;			
RT	"Molecular cloning of cyclic nucleotide-gated cation channel subunits			
RT	from pineal gland.";			
RL	Mol. Brain Res. 47:171-175(1997).			
RL	EMBL; AJ000496; CAA04133.1; -.			
DR	HSSP; O88703; IQ43.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005216; F:ion channel activity; IEA.			
DR	GO; GO:0005811; P:ion transport; IEA.			
DR	InterPro; IPR000595; cNMP binding.			
DR	InterPro; IPR005821; Ion trans.			
DR	Pfam; PF00027; cNMP binding; 1.			
DR	SMART; SM00520; Ion trans; 1.			
DR	PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN_1.			
DR	PROSITE; PS00889; cNMP_BINDING_2; 1.			
DR	PROSITE; PS50042; cNMP_BINDING_3; 1.			
KW	Ion transport; Ionic channel; Transmembrane; Transport.			
SEQ	SEQUENCE 1339 AA; 151046 MW; PFAD64A6A81AB49A CRC64;			
Query Match	46.3%;	Score 1959;	DB 2; Length 1339;	
Best Local Similarity	46.3%;	Pred. No. 1.8e-101;		
Matches 400; Conservative 121; Mismatches 240; Indels 102; Gaps 15;				
QY	11	VKPIGNNENSSRRNEEGSHPSNOSQQTAAQENKGBEKSILKTSKSTPTVTSBEPHTNIQ	70	
Db				
Db	512	IQGLPEEEKEEKEEKEE--EEKEEKEEKEEKEEKEEATNTVTPATKEHPELOVE	568	
QY	71	DKLSKKNSSGDLTUTPDQN-----AAEPTGTVP-----EKEMDPGK	108	
Db				
Db	569	DTDAAGALPIPETTIPPPRRPPVSPAKSDTLAVPSAATHRKPLPSQDDEAEELKALSPAE	628	
Db				

Qy 729 ENEDKGKE-NEDKDKGREPEKP-----LDRPECTASPIAVEEPHSPVRRVLP 776
Db 1165 DQHTHPKEAATDPAPRTPPPGSPSSPPAPSLGRPEEGEPA-EPEHSPVR----- 1218
Qy 777 RGTQRSLIISMAPSAGGEEVLTIEVKAKQ 809
Db 1219 -----ICMSPGPFGEQILSVKMPERE 1242

RESULT 7
CNG4 HUMAN
ID CNG4 HUMAN STANDARD; PRT; 909 AA.
AC Q14028; Q14029;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4)
DE (CNG4) (Cyclic nucleotide-gated cation channel modulatory subunit).
GN Name=CNG4; Synonyms=CNG4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
SEQUENCE FROM N.A. (ISOFORMS RCNC2A AND RCNC2B).
RC TISSUE=Retina;
RC MEDLINE=93226050; PubMed=7682292; DOI=10.1038/362764a0;
RA Chen T.Y., Peng Y.-W., Dhallan R.S., Ahmed B., Reed R.R., Yau K.-W.;
RT "A new subunit of the cyclic nucleotide-gated cation channel in
retinal rods";
RL Nature 362:764-767(1993).
CC -!- SUBUNIT: Heterooligomeric complex with CNG1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RCNC2B;
CC IsoId=Q14028-1; Sequence=Displayed;
CC Name=RCNC2A;
CC IsoId=Q14028-2; Sequence=VSP 001110;
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L15296; AAA65620.1; -;
DR EMBL; L15297; AAA65619.1; -;
DR Genbank; HGNC:2151; CNGB1.
DR MIM; 600724; -;
DR GO; GO:0017071; C:intracellular cyclic nucleotide activated c. . .; NAS.
DR GO; GO:0005222; F:intracellular cAMP activated cation channel. . .; NAS.
DR InterPro; IPR005595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel pore.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; Ion trans; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS0042; CNMP_BINDING_3; 1.
DR Multigene family; Transmembrane.
KW Alternative splicing; CAMP-binding; Ion transport; Ionic channel;
KW Multigene family; Transmembrane.
FT DOMAIN 1 314 Cytoplasmic (Potential).
FT TRANSMEM 315 333 H1 (Potential).
FT DOMAIN 334 347 Extracellular (Potential).
FT TRANSMEM 348 366 H2 (Potential).
FT DOMAIN 367 391 Cytoplasmic (Potential).

FT	TRANSMEM	392	411	H3 (Potential).
FT	DOMAIN	412	448	Extracellular (Potential).
FT	TRANSMEM	449	471	H4 (Potential).
FT	DOMAIN	472	515	Cytoplasmic (Potential).
FT	TRANSMEM	516	535	H5 (Potential).
FT	DOMAIN	536	619	Extracellular (Potential).
FT	TRANSMEM	620	640	H6 (Potential).
FT	DOMAIN	641	909	Cytoplasmic (Potential).
FT	DOMAIN	9	29	Poly-Glu.
FT	NP BIND	628	767	CAMP (By similarity).
FT	BINDING	688	700	CAMP (Potential).
FT	BINDING	700	700	CAMP (Potential).
FT	VARSPIC	1	286	Missing (in isoform RCNC2A).
FT	SEQUENCE	909 AA;	102285 MW;	/FTID=VSP_001110.
Qy	Query Match	46.0%;	Score 1949;	DB 1; Length 909;
Db	Best Local Similarity	46.2%;	Pred. No. 4e-101;	
Qy	Matches 403; Conservative 122;	Mismatches 238;	Indels 110;	Gaps 18;
Qy	14	IGENNENEQSRNEEGSHPSNQQTQAE--ENKGE--EKSLLTKTSPVTSEEPHTN	68	
Db	67	VGEAEKAEKAEKAEAEVAEAEKEPQDWAETKEEPEAEAEASSGVPAATKHQHEVQ	126	
Qy	69	IQDK-----LSKNSSGDLTTNPPQNAEPTGTVPQEKMDPGKEGN-----	112	
Db	127	VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLVPSASGTHRKKLPSEDDAEELK	184	
Qy	113	--SPQNKP-----PAAP-----	146	
Db	185	ALSPAESPVVAMSDPTTKDTGDQDRAASTASTNSAIIND-----VINEVADAQLHNLKVRQRTALY	240	
Qy	147	KKKLVEGDLs-----SPEASQTAKTAVPPVKGESDDKPT--EHYRLLWPKVKKMPLEY	200	
Db	241	KEKLDPDVTSDSESPKSPAKAPADPTKPAEAPVEEHEVCDMLCKCKFKHPWKY	300	
Qy	201	LKRIKLPNSIDSYDRLYLWLLVLTALYNWNCWFIPRLVFPYQTADNTHYWLADIIC	260	
Db	301	---QFPQSIDPLTNLMYVLMWLFVVMWNNCWLIPIVRWAFPYQTDPNTHHMLMDYLC	356	
Qy	261	DIILYDMLFIQRLQFVGGDIIVDSNELRKHVRTSTKFDLVASIIIPDICYLFQGN	320	
Db	357	DLIYFLDITVQRLQFVGGDIITDKQWRNNYLSRRFRMDLLSLDLFLYLKVGVN	416	
Qy	321	PMFRANMLKYTGFPEFNHLESIMDKAYIRYRITRTGYLLFILHINACYVYASNYEGI	380	
Db	417	PLRLPCLKYMAFFENFSRLESILSKAYYRVRTTAYLLYSLHNSCLYYASAQGL	476	
Qy	381	GTRRWYDGEENYLCYCYWAVRTLTITIGLPBPQTLFEIVFQLLNFPFVFSLLIGQ	440	
Db	477	GSTHWYDGVGNSYRCYFAVKTLITIGLPDPKTLFEIVFQLLNFTGCVAFSVMIGQ	536	
Qy	441	MRDVIQATANONYFRACMDDTTAYNNYSIPKLQKRVRTWYETWDSQRMDESLLK	500	
Db	537	MRDVGAATAGQTYRSCMDSTVKYMNFKYKIPKSVQNRVKTWYETWHSQMLDESLMV	596	
Qy	501	TLPTTVALAIDVNFISISKVDLFGCDTQMTYDMLRLKLSVLVLPFGDFVCKKEIGKE	560	
Db	597	QLPDKMLDLAIDVNNYIVSKVALFQCDQRMFLDKRLRSVVLVNDYVCKKEIGRE	656	
Qy	561	MYIKHGEVQLGPDGDKVLTILKAGSVFGEISLLAAGGNRRRTANVAHGFANLTLTD	620	
Db	657	MYIIQAGQVQLGPDGKSVLTLKAGSVFGEISLLAAGGNRRRTANVAHGFANLTLTD	716	
Qy	621	KYTLQELIHYVPSERILMKARVLKQAKTAETPRKDLALLFPKKEETPKLFTLL	680	
Db	717	KCOLNEILVHYPSQKLLRKARRMLSNK-----PKEEKSVLLIPPRAGTPKLFNAAL	771	
Qy	681	GGTGKAS-----LARIILKREQAOKENSEGEGEKEGKEDKQKEDKQK	728	
Db	772	AMTKMGKGKAGKGLAHLRLARUKELAALEAAKHEEL-----VEQAKSSQDVKGEGGAAP	828	
Qy	729	ENEDKGKE-NEDKDKGREPEKPILDRPECTASPIAV-----EESPFSVRRVLP	776	

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Db      829 DQTHPKAATDPAPRTPEPP-GSPSPSPASLGSCGEGPAEPESHSVR----- 882
QY      777 RGTSRQSLIISMAPSAGGEEVLTIETVEKAKO 809
Db      883 -----ICMSGPGEPGEQILSVKMPEREE 906

RESULT 8
Q9UMG2 Q9UMG2 PRELIMINARY; PRT; 1251 AA.
AC Q9UMG2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE CGMP-gated cation channel beta subunit.
GN Name=CNCG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96070429; PubMed=7590744;
RA Ardell M.D., Makhiya A.K., Oliveira L., Miniou P.,
RA Viegas-Pequignot E., Pittler S.J.;
RT "cDNA, gene structure, and chromosomal localization of human GARI
RT (CNCG3L), a homolog of the third subunit of bovine photoreceptor cGMP-
RT gated channel.";
RL Genomics 28:32-38(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96338110; PubMed=8766832; DOI=10.1016/0014-5793(96)00588-1;
RA Ardell M.D., Aragon I., Oliveira L., Porche G.E., Burke E.,
RA Pittler S.J.;
RT "The beta subunit of human rod photoreceptor cGMP-gated cation channel
RT is generated from a complex transcription unit.";
RL FEBS Lett 389:213-218(1996).
DR ENBL; U58837; AAB63387.1; -.
DR PIR; S69275; S69275.
DR HSSP; O88703; I043.
DR Gnew; HGNC:2151; CNGB1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; F:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR00595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1251 AA; 139604 MW; 4701C53DB13C9055 CRC64;

Query Match 46.0%; Score 1949; DB 2; Length 1251;
Best Local Similarity 46.2%; Pred. No. 6e-101;
Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;

QY 14 IGENNENQSRNRNEGHSPNSQQTQAE--ENKGE---EKSLTKSTPTVTSSEPHYN 69
Db 409 VGEAKKEAEKAEAEVAEEAEKPEQDWAETKEEPEAEAEAAASGGVPATKQHPVQ 468
QY 69 IQDK-----LSKKNSSGDLTTNPDPQNAEPTGTVPQEKENDPKGEPN----- 112
Db 469 VEUTDADCPDMAENPPS--TVLPSPSPAKSDTLVPSSASGTHRRKULPSEDDAEELK 526
```

beta subunit expressed in olfactory neurons.";

Proc. Natl. Acad. Sci. U.S.A. 95:4696-4701(1998).

[2]

SEQUENCE FROM N.A.

MEDLINE=99307326; PubMed=10377344;

Bonigk W., Bradley J., Muller F., Sesti F., Beekhoff I., Ronnett G.V., Kaupp U.B., Frings S.;

"The native rat olfactory cyclic nucleotide-gated channel is composed of three distinct subunits.";

J. Neurosci. 19:5332-5347(1999).

[3]

SEQUENCE FROM N.A.

Bonigk W., Sesti F., Bradley J., Ronnett G., Mueller F., Kaupp U.B., Frings S.;

Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

EMBL; AJ000515; CAA04152.1; --

EMBL; AF068572; AAC19120.1; --

HSSP; 088703; 1043.

GO; GO:0016021; C: integral to membrane; IEA.

GO; GO:0005216; F: ion channel activity; IEA.

GO; GO:0006811; P: ion transport; IEA.

InterPro; IPR000595; cNMP binding.

InterPro; IPR005821; Ion Trans.

Pfam; PF00027; cNMP binding; 1.

Pfam; PF00520; Ion Trans; 1.

SMART; SM00100; cNMP; 1.

PROSITE; PS00888; cNMP BINDING 1; UNKNOWN_1.

PROSITE; PS00889; cNMP BINDING_2; 1.

PROSITE; PS00842; cNMP BINDING_3; 1.

Ion transport; Ionic channel; Transmembrane; Transport.

SEQUENCE 858 AA; 96358 MW; 10B07CC41119F9A4 CRC64;

Query Match 45.4%; Score 1923; DB 2; Length 858;

Best Local Similarity 47.3%; Pred. No. 1.1e-99;

Matches 396; Conservative 114; Mismatches 228; Indels 100; Gaps 15;

QY 37 SQQTAAQENKGER-KSLKTKSTPTVTSSEPHNTIQDKLSKNSGDLTNPDPQN-----90

DB 53 SRRTALSNSFTKEIRSSIRRLVPATKEHPDELQVEDTDAEAGLPIPETIIPPPVSP 112

QY 91 AAETGTVP-----EKKMDPGK-----EGNPSQ-----NK 117

DB 113 AKSDTLAVPSAATHRKKLPSQDDAEELKALSPAESFVVAWSDPITTPQADGEDRAASTA 172

QY 118 PPAAPVINEYADAQHLNLRKMRQRTALYKKKLVEGDL-----SPASPTAKPTAVRPV 173

DB 173 SONSAIND-----RLQELVGNFKRTEKVAKEKIDPDVTSDEBSPKSPAKAPASAPAQ 228

QY 174 K--SSDDKPTHEYRLRFVKXKMPLETEYLKRIKLPSNSIDSYDRLYLWLLLVLTAYNW 231

DB 229 KPAEAAEAEHHCYDMLCKKRPWKY----QFPQSIDPLTNLWYLLWLVVLANWN 284

QY 232 NCWFIPRLVFPYQTADNIHWLIADIICDIYLYDMLFIQPLQVRGSDIIVDSNEUR 291

DB 285 NCWLIPVRWAFPYQRADNIHLMLDYLDFIYLLDITVFQMLQVRGSDIITDKKMR 344

QY 292 KHYRTSKFDLDVASIIPEDICVLFQFNPMFRANMLKYTSFERNHLESIMDKAYIT 351

DB 345 NNYLKSQRKMDLCLLPLDFLKLGVNPLLRPLCLTKMAPFNNRLEAILSKAYY 404

QY 352 RVIRTTGYLLFILHINACVYTWASNYBEGITTRWYVDGEGNEYLRCYVAVRTLTIGL 411

DB 405 RVIRTTAYLLSLHNSCLLYWASAFQIGSTHWYVDGVNSYIRCYVAVRTLTIGL 464

QY 412 PEPQTLFEIVPQLNFPFSGVVFSSLIGQMRDVIGAAATANQNYFRACMDDTIAYWNYSI 471

DB 465 PDPQTLFEIVFQLINLYETGVFAFSVMIGQMRDVVGAATAGQTYRSCMDSTVKYNFYKI 524

QY 472 PKLVOKERVRTWYETWDSQRMLESLLKTLPTTVQLALADIVNFSIIISKVLFGCDTQ 531

DB 525 PRSQNVKVTWYETWHSQGMDESLMWQLPDKMLDLDAIDVNYNIVSKVLFQCDRQ 584

QY 532 MIYDMLRLKSLVLPDGFCKKGEIGKENYIIKHGEVOVLGGPDGQTKVLTCLKAGSVFG 591

QY	153	GDLS	-----SPASPOAKPTAVPVK--ESDDKTEHYRLLWPKVKMPLTEYLKRIKL	206
Db	247	PDVTSDES	PKSPAKAPAPAPVKAQGVEEHYCEMLCKCFRRPWKKY-----QF	302
QY	207	PNSIDS	YDRLYLWLLVTLAYNNWCWFIPLRLVPFYQTADNIHYWLIADIICDIYLY	266
Db	303	QSIDPL	TNLMYILWLFVVLANNWCWLIPIVRWAFYQTPDNIHLWLLDYLCDLIYLL	362
QY	267	DMLFIQ	RLQFVRGGDIIVDSNELKHYRTSTKFDLVASIIIPDICYLPFGNPMFRAN	326
Db	363	DITVQMR	LQFVRGGDIITDKENRNKYVKSQRFMDMLCLLPDLLLYLKFVGNVPLRLP	422
QY	327	RMLKYS	TPFFNFHLESIMDKAYIYRVIRITGYLLFILHINACVYVWASNYEGIGTRWV	386
Db	423	RCLKYAF	FFENFNELESILSKAYYVIRITAYLLYSLHNSCLYWASAYEGLGSHWV	482
QY	387	YDGENY	LRICYWAVNTLITIGLPEPQTLFEIVFOLLNPFSGVVFSSLIQMRDVIG	446
Db	483	YDGVNS	YIRCYWAVKTLITIGLDPRTLFEIVFQGLNYFTGVFAFSVMIGQMRDVVG	542
QY	447	AATANQ	NYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMLEDLLKTLPTTV	506
Db	543	AATAGQ	TYRSCMDSTVKYMNFKIPRSVQNRVKTWYETWHSQGMDESELMVQPDKM	602
QY	507	QLALAI	DVNFISIISKVDLFGKCDTQMIYDMLLRKLSVLYLPQDFVCKKGIGKEMYIIKH	566
Db	603	RLDLAI	DVNYISVSKVALFOGCDRQMI FDKRLRSVVLYLPNDYVCKKGIGREMYIIQA	662
QY	567	GEVQVL	GGPGTKVLYTLKAGSVFGEISLLAAGGNRRRTANVAHGFPANLLTDKKTLOE	626
Db	663	QGVQLG	PGDGKSVLYTLKAGSVFGEISLLAAGGNRRRTANVAHGFTNLFILDKKOLNE	722
QY	627	ILVHYP	DSERILMKKARVLLKQAKTAEATPPKDLALLPPEKEETPKLTKLLGGTGKA	686
Db	723	ILVHYP	SQKLLRKARMLRNNK-----PKEKSVLILPPRAGTPKLFNAALAAAGKM	776
QY	687	SL	-----ARLLKREQAQKENSEGEEBEGKENEKQKENEKQKENEKDG	734
Db	777	GAKGRG	RLALLRLARLKEALAAARQQOL---LEQAKSSEDAAVGEE-----G	824
QY	735	KENEDK	DGKREPEKPLDRPECTA-----SPIAVEEHPHSVRTVLP	776
Db	825	SASPEQ	PRPEPEAPEAPEPTAPEPLAPEAPEAPAPSPSPASQERPEGDKAARP	884
QY	777	RGTSRQ	SLLIISMAPSABGGSEVLTIEVKEKAKQ 809	
Db	885	----	EEHPVRIHVTLGPPSPSEQILLVEVPEKQEE 914	
RESULT 11				
ID	O77659	PRELIMINARY;	PRT;	948 AA.
AC	O77659;			
DT	01-NOV-1998	(TReMBLrel. 08, Created)		
DT	01-NOV-1998	(TReMBLrel. 08, Last sequence update)		
DT	01-MAR-2004	(TReMBLrel. 26, Last annotation update)		
DE	Cyclic nucleotide-gated channel beta subunit id.			
GN	Name=CNCbeta;			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98345361; PubMed=9679145; DOI=10.1083/jcb.142.2.473;			
RA	Wiesner B., Weiner J., Middelendorff R., Hagen V., Kaupp U.B.,			
RT	Weyand I.;			
RT	"Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry			
RT	into sperm.";			
RL	J. Cell Biol. 142:473-484 (1998).			
DR	EMBL; AF074013; AAC26128.1; -.			

DR	HSSP; O88703; 1Q43.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005216; F:ion channel activity; IEA.			
DR	GO; GO:0006811; P:ion transport; IEA.			
DR	InterPro; IPR000595; cNMP binding.			
DR	InterPro; IPR005821; Ion trans.			
DR	Pfam; PF00027; cNMP binding; 1.			
DR	Pfam; PF00520; Ion trans; 1.			
DR	SMART; SM00100; cNMP; 1.			
DR	PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.			
DR	PROSITE; PS00889; CNMP_BINDING_2; 1.			
DR	PROSITE; PS00042; CNMP_BINDING_3; 1.			
KW	ion transport; Ionic channel; Transmembrane; Transport.			
SQ	SEQUENCE 948 AA; 105211 MW; 1DA77400115C2074 CRC64;			
	Query Match 45.3%; Score 1920; DB 2; Length 948;			
	Best Local Similarity 45.9%; Pred. No. 1.8e-99;			
	Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;			
QY	15	GENNEQSSRRNEEGSHPSNQSQQTAAQENKGEKSLKTSKSTPVTSEPHNTIQDK--	72	
Db	86	GAQAQGEVGAQEQDQVGGA-QDQSTSHQELQ--EALADSSGVPAEEHPELOVEDADA	142	
QY	73	-----LSKNSSGDLTTNPDPPQNAEPTGTVP-----EQKEMDPGK 108		
Db	143	DSRPLIABENPPSPVQLPSP--AKSDTLAVPGSATGSLRKRLPSQDDAEABELKMLSPA	200	
QY	109	-----EGPNSQNKPPA-----APVINEYADAQLHNLVKEMRORTALYKKKLVE 152		
Db	201	SPVAVMSDDTSPQDQDDQDRATSTASQNSAIIND---RLQELVKLFKERTKVEKELID 256		
QY	153	GDLS-----SPEASPOAKPTAVPVK--ESDDKPTHEYRLLWFKVKMPLTEYLKRIKL 206		
Db	257	PDVTSDEESPSPAKKAPAPAPVKAQGVVEEHYCEMLCKCFRRPWKKY-----QF 312		
QY	207	PNSIDSYDRLYLWLLVTLAYNNWCWFIPLRLVPFYQTADNIHWLIADIIIDIYLY 266		
Db	313	QSIDPLTNLMYILWLFVVLANNWCWLIPIVRWAFYQTPDNIHLWLLMDYLCDLIYLL 372		
QY	267	DMLFIQRLQFVRGGDIIIVDSNELKHYRTSKFDLDVASIIPDFICYLPFGGNPMFRAN 326		
Db	373	DITVFMRLQFVRGGDIITDKEMRNKYVKSQRFMDMLCLLPDLLLYLKFVGNPLRLP 432		
QY	327	RMLKYTSFFEFNFHLESIMDKAYIYRVIRITGYLLFILHINACVYVWASNYEGIGTRWV 386		
Db	433	RCLKYMAFFEFNRLLESILSKAYYVIRITAYLLYSLHNSCLLYWASAYEGLGSHWV 492		
QY	387	YDGENYLRICYWAVNTLITIGLPEPQTLFEIVFOLLNPFSGVVFSSLIQMRDVIG 446		
Db	493	YDGVGNSYIRCYWAVKTLITIGLDPRTLFEIVFQGLNYFTGVFAFSVMIGQMRDVVG 552		
QY	447	AATANQNYFRACMDDTIAYNNYSIPKLQKVRVTWYETWDSQRMLEDSDLLKTLPTTV 506		
Db	553	AATAGQTYRSCMDSTVKYMNFKIPRSVQNRVKTWYETWHSQGMDESELMVQPDQK 612		
QY	507	QLALAIQVNFISIISKVDLPFGCDTQMIYDMLLRKLSVLYLPQDFVCKKGIGKEMYIIKH 566		
Db	613	RLDLAIQVNYISVSKVALFOGCDRQMI FDKLRLRSVVLYLPNDYVCKKGIGREMYIIQA 672		
QY	567	GEVQVLGGPDGKTVLYTLKAGSVFGEISLLAAGGNRRRTANVAHGFPANLLTDKKTLOE 626		
Db	673	QGVQVLGGPDGKSVLYTLKAGSVFGEISLLAAGGNRRRTANVAHGFTNLFILDKKOLNE 732		
QY	627	ILVHYPDSERILMKKARVLLKQAKTAEATPPKDLALLPPEKEETPKLTKLLGGTGKA 686		
Db	733	ILVHYPESQKLLRKARMLRNNK-----PKEKSVLILPPRAGTPKLFNAALAAAGKM 786		
QY	687	SL-----ARLLKLRQEAQKENSEGEEKENEKQKENEKQKENEKDG 734		
Db	787	GAKGRGGELALLRLARLKEALAAARQQOL---LEQAKSSEDAVGEE-----G 834		
QY	735	KENEDKDGKREPEKPLDRPECTA-----SPIAVEEHPHSVRTVLP 776		

RC TISSUE=Retina;
 RA PubMed=2014230;
 RX Sugimoto Y., Yatsunami K., Tadjimoto M., Khorana H.G., Ichikawa A.;
 RA "The amino acid sequence of a glutamic acid-rich protein from bovine
 RT retina as deduced from the cDNA sequence."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3116-3119(1991).
 CC -|- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Isoform CNG4D is the most frequent isoform
 CC (CNG4D:CNG4C:CNG4E = 20:2:1) in testis;
 CC Name=CNG4C;
 CC IsoId=Q28181-1; Sequence=Displayed;
 CC Name=CNG4D;
 CC IsoId=Q28181-2; Sequence=VSP_001109;
 CC Name=CNG4E;
 CC IsoId=Q28181-3; Sequence=VSP_001108;
 CC -|- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
 CC -|- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X89626; CAA61769.1; -;
 DR EMBL; X94707; CAA64367.1; -;
 DR EMBL; M61185; AAA30536.1; -;
 DR PIR; A40437; A40437.
 DR Reactome; Q28181; -;
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion Trans.
 DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00520; Ion Trans; 1.
 DR PROSITE; PS00888; cNMP BINDING_1; 1.
 DR PROSITE; PS00889; cNMP BINDING_2; 1.
 DR PROSITE; PS50042; cNMP BINDING_3; 1.
 KW Alternative splicing; cAMP-binding; Direct protein sequencing;
 KW Ion transport; Ionic channel; Multigene family; Transmembrane.
 FT CHAIN 1 590
 FT 454 1394
 FT DOMAIN 1 770
 FT TRANSMEM 771 789
 FT DOMAIN 790 803
 FT DOMAIN 804 822
 FT TRANSMEM 823 847
 FT DOMAIN 868 904
 FT TRANSMEM 905 927
 FT DOMAIN 928 971
 FT TRANSMEM 972 991
 FT TRANSMEM 992 1075
 FT TRANSMEM 1076 1096
 FT DOMAIN 1097 1394
 FT NP BIND 1084 1222
 FT BINDING 1144 1144
 FT BINDING 1156 1156
 FT CARBOHYD 1067 1067
 FT VARSPPLIC 515 532
 FT 522
 FT VARSPPLIC 530
 FT 341
 FT CONFLICT 454 465
 FT CONFLICT 482 482
 FT CONFLICT 499 499
 FT CONFLICT 572 590
 VPATEBHEPELQVEDADADS -> GSFQMSPFALQCEALUK

FT CONFLICT 1283 1283 R (in Ref. 3).
 FT CONFLICT 1289 1289 S -> A (in Ref. 2).
 FT CONFLICT 1336 1336 R -> A (in Ref. 2).
 FT CONFLICT 1338 1338 D -> E (in Ref. 2).
 FT CONFLICT 1338 1338 A -> AA (in Ref. 2).
 SQ SEQUENCE 1394 AA; 155064 MW; EE6DA559BE3744A7 CRC64;
 Query Match 45.3%; Score 1920; DB 1; Length 1394;
 Best Local Similarity 45.9%; Pred. No. 3e-99;
 Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;
 QY 15 GENNENEQSRNNEEGSHPSNQSOQTAAQENKNGEKSILKTSPTVTSPEPHNIODK-- 72
 DB 532 GAQAQGEVGAQEQDGVGGA-QDQSTSHQELQ--EALADSSGVGPATEBHEPELQVEDADA 588
 QY 73 -----LSKKNSSGDLTTNPDQNAAEPTGTVP-----BQKENDPGK 108
 DB 589 DSRPLIAEENPPSPVOLPLSP--AKSDTLAVPGSATGSRKLRLPSODDEAEELKMLSPAA 646
 QY 109 -----EGNPSQNKPPA-----APVINEYADAQHLNFKRMORTALYKKKLVE 152
 DB 647 SPVAMSDFTSQGTDDQDRATSTASQNSAIIND-----RLQELVKLFKERTKVKLELD 702
 QY 153 GDLS-----SPEASPTAKPTAVPPVK--ESDDKTEHYRLLWFKVKMPLTEYLKRIKL 206
 DB 703 PDVTSDEESPKSPAKAPAPAEVKAAGOVVEEHYCEMLCCKPKRPPWKY-----QF 758
 QY 207 PMSIDSYDRLVLLMLLTLAVNNCWFIPLRLVFPYQTDNIHNYMLADIICDIILY 266
 DB 759 POSIDPLTNMLYILMLFFVLLANNWNCWLIPLVRAPFYQTPDNILHMLMDVLCDIILY 818
 QY 267 DMLFTQPLQFVRGGDIIVDSNELKRYHRTSTKFDLVAISIIPFDCILFFGFNPMFRAN 326
 DB 819 DITVQMRLOFVRGGDIITDKKEMNNYVKSQRFKMDMLCLPLDLLLYLKFGVNPPLRLP 878
 QY 327 RMLKYSFPFENHLESIMDKAYIRVIRTTGYLLFILHINACVYVWASNYEGIGTRWV 386
 DB 879 RCLKYMAFPEFNRLSILSKAYVVRVIRTTAYLLYSLHNSCLYVWASAYEGLGTHWV 938
 QY 387 YDGEQNEVLCYVWAVRVLITIGGLPEPOTLFEIVFOLLNFFSGVVFSSLLQMEDVLG 446
 DB 939 YDGVGNSYIRCYVWAVKTLITIGGLPDPRLFEIVFQGLNYFTGVFAFVMLGQMRDVG 998
 QY 447 AATANQYFRAQWDDTIATMNNYSIPKLQKQVRYWYETWDSQRMLEDSDLLKTLPTTV 506
 DB 999 AATAGTYVRSQWDSVTKVMFYKIPRSVQNRVKTWYETWHSQGMDESELVQLPDKM 1058
 QY 507 QALALDVNFISIISKVDLPKGCOTQMYDMLRLKSVLYLPGDFVCKGGEIKEMVILKH 566
 DB 1059 RLDLAIDVNSYISVSKVALFQGCGRQIMFDMLKRLRSVVYLPNDVYVCKGGEIGREMYIIQA 1118
 QY 567 GEVOVLGGPDGTVLVTLKAGSVFGEISLLAAGGNGRRTANVVAHGFANLLTLDKKTLOS 626
 DB 1119 GQVQLGGPDGKSVLTLKAGSVFGEISLLAAGGNGRRTANVVAHGFANLLTLDKKTLOS 1178
 QY 627 ILVHPDSEIRIIMKKARVLLKQAKTAEATPPRKLALIFPPKEETPKLFTLLGGTGKA 686
 DB 1179 ILVHPESQKLKRRKARMLRNNK-----PKEKSVLILPPRAGTPKLFNLAALAAAGKM 1232
 QY 687 SL-----ARLLKPKRQAQAKENEGEGEOKENEDKQENEDKQENEDKQENEDKQ 734
 DB 1233 GAKGGGRGLALLRLARLKLAAALAAARQQQL---LEQAKSDEDAARVGE-----G 1280
 QY 735 KENEDKDKGREPEKPLDRPECTA-----SPTAVEEPHSVRRTVLP 776
 DB 1281 SASPPQPPPEPAP 1340
 QY 777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
 DB 1341 ---EEHPVRIHVTGLGDPSEQLLVEVPEKQEE 1370
 RESULT 14

Q9W2D5 Q9W2D5 PRELIMINARY; PRT; 1040 AA.
AC Q9W2D5; Q8IH43;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE CR17922-PA (GH25102p).
GN ORFNames=CG17922;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Buzan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Hradecky P., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Plattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RX EMBL; AE003454; AF46757.2;
DR EMBL; BT001439; AAN71194.1;
DR HSSP; O88703; IQ3E.
DR FlyBase; FBgn0034636; CG17922.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; P: ion channel activity; IEA.
DR GO; GO:0005267; P: potassium channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR GO; GO:0006813; P: potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00027; CNMP-binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00889; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; UNKNOWN_1.
DR PROSITE; PS00842; CNMP_BINDING_3; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1040 AA; 118713 MW; 4A643FDA21D2D5B8 CRC64;
Query Match 26.1%; Score 1103; DB 2; Length 1040;
Best Local Similarity 33.4%; Pred. No. 1.6e-53;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;
Oy 16 ENNEGSSRRNEEGSHPSNQSOQTAA-----EENKGEKSLTKSTPTVTSSEPTNI 69
Db 279 EEEEEKSSFLHQLVQESQDVEDQVQICYNSEPELQNEEDNRNRTQRTPSINESEIVAV 338
Oy 70 QDKLSKNSGDLTTNPDPQNAEPTCTVPEQEMDPGKSPNQKPPAAPVINEYAD 129
Db 339 DEPDTEWNSVDV---HRKPSSA-----GSLDSQGG-----QFLR 369
Oy 130 AQLHLNLYKRMQRORTALYKKKLVEGDLSSPEASQPTAKPTAVPPVKESDDKPTHEYRLW 189
Db 370 DQVRLVRRRTARANKVKSRI---ELPPTSSSTVSSPPPTKSLHPSP-QH----- 419
Oy 190 FKVKMPLTEYLKRIKU-----PNSIDSYD-----RLYLWLLVLLVTLA 228
Db 420 -KVLVPAGSPHGRFLFEADTPRSNVWLCSSLCGANNDBRTLDPOGKIYISMLCVVSL 478

Qy	229	YNNWCWFIPLRLVFPYQYADNIHLYLIADICDIILYDMLFIQPRLOFVRGGDIIVDSN	288
Db	479	FLYNARWVPLRASPFPQTKENTNWLACDCADIIYLLDVFFKHRVMYLFEGFWKKN	538
Qy	289	ELRKHYSYTSKQOLDVASIIPDCIYLPFGNPMF-RANRMLKYTSFPFNHLESIMDK	347
Db	539	LTRKNYMRKLQKLDLLALLPLELLYFKLGQTQAVWLFRPFRFKTQSPWEVFRLLDRVISS	598
Qy	348	AYIVRVTRTGYLLFIILHINACVYMASNYEGITRWVYDGGNEVLCYCYNAVRTLIT	407
Db	599	PHFVRVAKTLTYMLYMIHTAALYIAYSDYQGLQGNRWVFGSGHPYRCFAFATKTATS	658
Qy	408	IGGLPEPQTLFEIVFOLLNFFSGVVFSSLIGOMRDVIGAAATANQNYFRACMDDTIAYMN	467
Db	659	IGKNPKPERQGEYVMTVAMLGVFVALLIGIRDIISTATRNKHEYRQLEDETLEYMR	718
Qy	468	NYSIPKLVQKRVTRTWYTWDSQRMLESLLKTLPTTVQALAIADVNFISIKVDLPKG	527
Db	719	RLNLSQEVQSRVKNWFQFTWEQORTLDESILDALPINKLTDIAISVHIQTLISKVQLFAD	778
Qy	528	CDTQMIYDMLRLKSLVLYLPQDFVCKKGEIGKEMYIIKHGEVOVLGGPDGTKVLVTLKAG	587
Db	779	CERALLDLKURAVTFLPQDFVCRKGEVGREMIIVKLGQVQVMGGPSSDVVLATITEG	838
Qy	588	SFVGEISLLAAGGNRRRTANVVAHGFANLLTLDKKTILQEIIVHYPOSERILMKKARVLL-	646
Db	839	SFVGEISLLGINGADRRTADVRSKGSYNSLVLSKSDLNEVIAYPYTAQALLKXRAQLMR	898
Qy	647	KQAKATBAATPPKDLAL-----LFPK--EETPKLFTLLGGTGKASLARLLKLKREQA	699
Db	899	KNAAREERERARSALQADVIGNPKTPETAPKLQTVIQAIPFESPAVLITRGSKR	958
Qy	700	AQKENS 706	
Db	959	MRRKQOS 965	
RESULT 15			
ID	P90975	PRELIMINARY; PRT; 800 AA.	
AC	P90975		
DT	01-MAY-1997	(TrEMBLrel. 03, Created)	
DT	01-MAY-1997	(TrEMBLrel. 03, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Cyclic nucleotide-gated channel.		
GN	Namestax-2;		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97048185; PubMed=8893026; DOI=10.1016/S0896-6273(00)80201-9;		
RA	Coburn C.M., Bargmann C.I.;		
RT	"A putative cyclic nucleotide-gated channel is required for sensory		
RT	development and function in C. elegans.";		
RL	Neuron 17:695-706(1996).		
DR	ENBL; U73476; AAB41492.1; --		
DR	HSSP; O88703; IQ3E.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005216; F:ion channel activity; IEA.		
DR	GO; GO:0005267; F:potassium channel activity; IEA.		
DR	GO; GO:0006811; P:ion transport; IEA.		
DR	GO; GO:0006813; P:potassium ion transport; IEA.		
DR	InterPro; IPR000595; cNMP binding.		
DR	InterPro; IPR005821; Ion channel.		
DR	InterPro; IPR001622; K+channel pore.		
DR	Pfam; PF001202; WW Rep5 WWP.		
DR	Pfam; PF00027; cNMP binding; 1.		
DR	Pfam; PF00520; Ion Trans; 1.		
DR	SMART; SM00100; cNMP; 1.		
DR	PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.		

DR	PROSITE; PS00889; CNMP_BINDING_2; UNKNOWN_1.		
DR	PROSITE; PS00442; CNMP_BINDING_3; 1.		
DR	PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.		
KW	Ion transport; Ionic channel; Transmembrane; Transport.		
SQ	SEQUENCE 800 AA, 92462 MW, D0498AD2C340PDAA CRC64;		
Qy	Query Match 25.9%; Score 1096; DB 2; Length 800;		
Db	Best Local Similarity 31.5%; Pred. No. 2.9e-53;		
Qy	Matches 253; Conservative 146; Mismatches 301; Indels 102; Gaps 19;		
Qy	26 RNEEGSHPSNQSQTTAQBENKG-----EKSILKTKSTPTVSEPHNTIQDKLSKKNSSG	80	
Db	17 RKREFSYDVRQAKRPTQLSEKGSPPRSEDSFDLLDPANASKEP-----	61	
Qy	81 DLTTNPDQNAAEP-----TGTVPEQKE-----MDPGKSGPNSPONKPPA	120	
Db	62 SASTRELPPYPTPRPEVVIQIDEVSPILGLIDETDDHDLGRDLDPASSFDANSLSATRA	121	
Qy	121 APVINEYADAQ-----LHNLVKRMQRORTALYKKGVEGLSSPEASPOKTAPVAPP	172	
Db	122 SSIIEDDVRSQISFTMRERLHLSIAKEVHRRTSAVREDLIR---ETPEDTVSMA--SNVP-	175	
Qy	173 VKESDDKPTHEYRLLWLFVKV-KMPLTEYLKR---IKLPNSIDSYTDRLLYLWLLVTLA	228	
Db	176 -KQNEHRPS--LMSLIGLQNRSESPVTDTVKNCFCFSLKGTTHPY-GRFYMTWLSLVTL	231	
Qy	229 YNNWCWFIPLRLVFPYQYADNIHLYLIADICDIILYDMLFIQPRLOFVRGGDIIVDSN	288	
Db	232 FLFNACFILPRSYPYQYADNMWYFIVDYSCDLYVIDMLLIKPLRTRGGIQVKYK	291	
Qy	289 ELRKHYSYTSKQOLDVASIIPDCIYLPFGNPMFRANRMLKYTSFPFNHLESIMDKA	348	
Db	292 DTQRHYLWTRTEFKDILSILPTDLMYFFPGKMPWRINRVLKNSEFWLLDFMLDNSFANP	351	
Qy	349 YIVRVIRITGYLLFIILHINACVYMASNYEGIG-----TTRWYVDGEGNEYLCR	397	
Db	352 YAIRARTLSYMIYIIHCNCSVYKLSALQAQFGQIAYLENGKWYLNKWNQGNAYIRC	411	
Qy	398 YVMVAVRTLITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIIGMRDVI GAATANQNYFRA	457	
Db	412 FFYTAATAVATSTGNNAFTNVIYIYNTCSMMGVFVALLLQIRDIVSNANRNEEFQR	471	
Qy	458 CMDDTIAMNNYSIPKLQKRVTRTWYTWDSQRMLESLLKTLPTTVQALAIADVNFSS	517	
Db	472 KMDLALGECKLGLKMETTRVRDWFIVTQQQKTLDEKKLIEKLPKLQTLALSVHYT	531	
Qy	518 IISKVDLPKGCDDTQMIYDMLLKLKSVLYLPQDFVCKKGEIGKEMYIIKHGEVOVLGG	577	
Db	532 TLSKVQLFQDCDRALLRLDLKLRPVIFLPGDMI CLKGDVGKEMYIINQGIQLQVVGDN	591	
Qy	578 TKVLVTLKAGSVFGEISLLAAGGNRRRTANVVAHGFANLLTLDKKTLOBILVHYPSERI	637	
Db	592 EKIFAEIAGQAVFGEISLLAAGGNRRRTASIRAKGYCTLFVLAKEDLNDVIRYPOAQT	651	
Qy	638 LMKARVLLKQAKATAEATPPRKDLALL-----FPPKEETPKLFTLLGGT-----GKA	686	
Db	652 LRRKAAAMLKNDKSKDEKTEKIKAQAELEDRCCKINPR-QVPKLITLIANNTEWENKGVQ	710	
Qy	687 SLARLLKLKREQAAQK-----ENSEGGEEBEGKENEKQKENEK-----KQKENEK	732	
Db	711 ELKKVIEEETEKSRQSIYYPWSTLQRODDDEEWNDEDLSDVGDEDFDLPNTNHSDD	770	
Qy	733 KGKENEKDKGREPEEKPLDRP 754		
Db	771 ---PMEDVDLAEVHDDWDQD 789		

Search completed: March 27, 2005, 20:58:12
Job time : 136 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 03:59:35 ; Search time 10099 Seconds
(without alignments)
11659.191 Million cell updates/sec

Title: US-09-855-828-3

Perfect score: 2430

Sequence: 1 atgtttaatcgtgacaaa.....aagaaaggctaagcaataa 2430

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_at.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2430	100.0	4369	9 AF272900	AF272900 Homo sapi
2	2049.4	84.3	2135	9 AF228520	AF228520 Homo sapi
3	1682.2	69.2	2826	4 AF490511	AF490511 Canis fam
4	1362.4	56.1	4710	10 MMU243572	AJ243572 Mus muscu
5	853.4	35.1	1350	6 CQ716885	CQ716885 Sequence
6	577.4	23.8	3025	9 HUMCNGCB	L15297 Homo sapien
7	577.4	23.8	3408	9 HUMCNGCCA	L15296 Homo sapien
8	577.4	23.8	4033	9 HSU58837	U58837 Human cGMP-
9	577.4	23.8	4382	9 AF074298	AF074298 Homo sapi
10	575.8	23.7	4320	6 CQ715550	CQ715550 Sequence
11	575.2	23.7	4763	10 BC045114	BC045114 Mus muscu
12	572.2	23.5	3083	4 AF074012	AF074012 Bos tauru
13	572.2	23.5	3090	4 AF074013	AF074013 Bos tauru
14	572.2	23.5	3253	4 BFCNG4CGN	X94707 B.taurus mR
15	572.2	23.5	3290	4 AF074014	AF074014 Bos tauru
16	572.2	23.5	4282	4 BTRPCNGCL	X89626 B.taurus mR
17	569.6	23.4	4238	10 RNCNG41	AU000496 Rattus no
18	568	23.4	3236	6 CQ880122	CQ880122 Sequence
19	568	23.4	3236	10 RNCNG43	AJ7000515 Rattus no

20	568	23.4	3328	10 AF068572	AF068572 Rattus no
21	330	13.6	205816	9 AC013751	AC013751 Homo sapi
22	237.4	9.8	2511	3 CEU73476	U73476 Caenorhabdi
23	223	9.2	3275	6 CQ598668	CQ598668 Sequence
24	223	9.2	3358	3 BT001439	BT001439 Drosophil
25	217.8	9.0	3099	10 BC046523	BC046523 Mus muscu
26	196.2	8.1	441	10 AF015728	AF015728 Rattus no
27	187.4	7.7	1709	3 AY060725	AY060725 Drosophil
28	181.2	7.5	2061	4 SSU85404	U85404 Sus scrofa
29	181.2	7.5	2487	6 CQ716337	CQ716337 Sequence
30	181.2	7.5	2857	9 S42457	S42457 CNGG=rod ph
31	176.8	7.3	2697	4 CFACGMP	X99114 C.familiar
32	176.8	7.3	2717	4 CFU83905	U83905 Canis famil
33	176.4	7.3	2500	6 AX930698	AX930698 Sequence
34	176.4	7.3	2500	9 HUMCGRP	M84741 Human cGMP-
35	173.6	7.1	2682	4 BFCGMPCH	X51604 B.taurus RN
36	169.8	7.0	1674	9 AF547222	AF547222 Homo sapi
37	169.8	7.0	181804	9 AC107068	AC107068 Homo sapi
38	166.4	6.8	2297	10 MMU19717	U19717 Mus musculu
39	164.8	6.8	2474	10 MUSCNGC	M84742 Mus musculu
40	162.4	6.7	6312	3 AF091302	AF091302 Limulus p
41	161.4	6.6	58409	10 AL772281	AL772281 Mouse DNA
42	155.6	6.4	2612	5 GGRDCCG	X89599 G.gallus mR
43	155.4	6.4	68732	2 AC151330	AC151330 Xenopus t
44	152	6.3	2052	10 RNU48803	U48803 Rattus norv
45	150.6	6.2	200535	10 AL671880	AL671880 Mouse DNA

ALIGNMENTS

RESULT 1	AF272900	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel	4369 bp mRNA linear PRI 29-AUG-2000
LOCUS	AF272900		
DEFINITION	AF272900	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel	
ACCESSION	AF272900		
VERSION	AF272900.1	GI:9247065	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
CDS			

Db	1907	AAAAAGACCCCTCAAGAAAATCTTAGTGCATATATCCAGATTCTGAAGAGATCTCATGAAG	1967
Qy	1921	AAAGCCAGAGTGCTCTTTTAAAGCAGAAAGGCTAAAGACCCGAGAACCCCTCCAAAGAAAA	1980
Db	1967	AAAGCCAGAGTGCTCTTTTAAAGCAGAAAGGCTAAAGACCCGAGAACCCCTCCAAAGAAA	2026
Qy	1981	GATCTTGCCCTCTCTTCCACCGAAAGAGACACCCAAAATCTGTTTAAAACTCTCCCTA	2040
Db	2027	GATCTTGCCCTCTCTTCCACCGAAAGAGACACCCAAAATCTGTTTAAAACTCTCCCTA	2086
Qy	2041	GGAGGCACAGAAAGCAAGTCTTTCGAAGACTACTCAAAATGGAAGCGAGAGCAAGCGCT	2100
Db	2087	GGAGGCACAGAAAGCAAGTCTTTCGAAGACTACTCAAAATGGAAGCGAGAGCAAGCGCT	2146
Qy	2101	CAGAAGAAAGAAAATCTTGAAGGAGAGAGGAAGAAAAGAAAATGAAGATATAACAA	2160
Db	2147	CAGAAGAAAGAAAATCTTGAAGGAGAGAGGAAGAAAAGAAAATGAAGATATAACAA	2206
Qy	2161	AAAGAAAATGAAGATAAACAAAAGAAAATGAAGATAAGAGAAAATGAAGATAAA	2220
Db	2207	AAAGAAAATGAAGATAAACAAAAGAAAATGAAGATAAGAGAAAATGAAGATAAA	2266
Qy	2221	GATTAAGGAAGAGAGCCAGAGAGAGAGCCACTGGACAGACCTGATGTACAGCAAGTCCT	2280
Db	2267	GATTAAGGAAGAGAGCCAGAGAGAGAGCCACTGGACAGACCTGATGTACAGCAAGTCCT	2326
Qy	2281	ATTGCAGTGAGGAAGAACCCCACTCAGTTTAGAAGGACAGTTTTACCCAGAGGACTTCT	2340
Db	2327	ATTGCAGTGAGGAAGAACCCCACTCAGTTTAGAAGGACAGTTTTACCCAGAGGACTTCT	2386
Qy	2341	CGTCAATCACTCATTTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGGTTCTTACT	2400
Db	2387	CGTCAATCACTCATTTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGGTTCTTACT	2446
Qy	2401	ATTGAACTCAAGAAAAGGCTTAAGCAATAA	2430
Db	2447	ATTGAACTCAAGAAAAGGCTTAAGCAATAA	2476
RESULT 2			
LOCUS	AF228520	2135 bp	mRNA linear PRI 30-JUN-2000
DEFINITION	Homo sapiens cone photoreceptor cGMP-gated cation channel		
ACCESSION	AF228520		
KEYWORDS	AF228520.1 GI:8843947		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Sundin,O.H., Yang,J.M., Li,Y., Zhu,D., Hurd,J.N., Mitchell,T.N., Silva,E.D. and Maumenee,I.H.		
TITLE	Genetic basis of total colourblindness among the Pingelapese islanders		
JOURNAL	Nat. Genet. 25 (3), 289-293 (2000)		
MEDLINE	20347712		
PUBMED	10888875		
REFERENCE	2 (bases 1 to 2135)		
AUTHORS	Sundin,O.H., Yang,J.-M., Li,Y., Zhu,D., Silva,E.D. and Maumenee,I.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-JAN-2000) Ophthalmology, Johns Hopkins School of Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA		
FEATURES	Location/Qualifiers		
source	1..2135		
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	/mol_type="mRNA"		
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	/chromosome="8"		
	/map="8q21-q22"		
	/tissue type="retina"		

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Qy 1120 GCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGAAGGAACGAG 1179
Db 781 GCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGAAGGAACGAG 840
Qy 1180 TATCTGAGATGTTTATTTGGGCAAGTTCGAACCTTTAAATTAACCATTTGGTGGCTTCCAGAA 1239
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Db 901 CCACAACTTTATTTGGAATTTGTTTCAACTCTTGGAATTTTTTTTCTGAGTTTTTGTG 960
Qy 1300 TTCTCCAGTTTAAATTTGGTTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCAAATCAGAAC 1359
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Qy 1420 CTTGTGCAAAAGAGTTTCGACCTTGTGATGATATATACATGAGGACTCTCAAGAAATGCTA 1479
Db 1081 CTTGTGCAAAAGAGTTTCGACCTTGTGATGATATATACATGAGGACTCTCAAGAAATGCTA 1140
Qy 1480 GATGAGTCTGATTTGCTTAAAGACCTACCAACTACGGTTCAGTTAGCCCTCGCCATTGAT 1539
Db 1141 GATGAGTCTGATTTGCTTAAAGACCTACCAACTACGGTTCAGTTAGCCCTCGCCATTGAT 1200
Qy 1540 GTGAACCTTACGATCATCAGAAAGTCAGCTTGTTCAGGGTTGTGATACACAGATGAT 1599
Db 1201 GTGAACCTTACGATCATCAGAAAGTCAGCTTGTTCAGGGTTGTGATACACAGATGAT 1260
Qy 1600 TATGACATGTTGCTTAAGATGAAATCCGTTCTCTATTGCTCGTGCATTTGTCTGCAA 1659
Db 1261 TATGACATGTTGCTTAAGATGAAATCCGTTCTCTATTGCTCGTGCATTTGTCTGCAA 1320
Qy 1660 AAGGAGAAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAGTCCAAGTTCTTGGGA 1719
Db 1321 AAGGAGAAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAGTCCAAGTTCTTGGGA 1380
Qy 1720 GGCCCTGATGGTACTAAAGTTCTGTTTACTCTGAAGCTGGGTGGTGGAGAAATC 1779
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Qy 1840 GCCAATCTTTTAACTCTAGACAAAAAGACCCCTCCAAGAAATTTCTAGTGCATTAATCCAGAT 1899
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Db 1546 TCTGAAGAGTCTCTATGAAGAACCCAGAGTCTTTTAAAGCAGAGGCTTAAGCCGGA 1605
Qy 1960 GAAGCAACCCCTCCAAGAAAGATCTTGCCCTCTCTTCCACCCGAAAGAGACACCC 2019
Db 1606 GAAGCAACCCCTCCAAGAAAGATCTTGCCCTCTCTTCCACCCGAAAGAGACACCC 1665
Qy 2020 AAATGTTTAAAACTCTCTAGAGGACACAGGAAAAAGCAAGTCTTCCAAGACTACTCAA 2079
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Qy 2080 TTGAAGGAGGACAGAGCTCAGAGAAAGAAATTTCTGAAGGAGGAGGAGGAGGAGGA 2139
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Qy 2140 AAAGAAAATCAAGATAAACAAGAAAATGAAGATAAACAAGAAAATGAAGATAA 2199
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Qy 2260 CTTGAATGTACAGCAAGTCTTATTTGAGTGGAGGAAGAACCCCACTCAGTTAGAAGACA 2319
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Qy 2320 GTTTTACCAGAGGAGTCTCTGTCATCACTCACTTATCAGCATGCTCTTCTGCTGAG 2379
Db 1966 GTTTTACCAGAGGAGTCTCTGTCATCACTCACTTATCAGCATGCTCTTCTGCTGAG 2025
Qy 2380 GCGGAGAGAGAGTCTTCTACTATTGAAGTCAAGAAAAGGCTTAAGCAATAA 2430
Db 2026 GCGGAGAGAGAGTCTTCTACTATTGAAGTCAAGAAAAGGCTTAAGCAATAA 2076

RESULT 3
AF490511 2826 bp mRNA linear MAM 31-JUL-2002
LOCUS
DEFINITION
Canis familiaris cyclic nucleotide gated channel beta subunit
(CNGB3) mRNA, complete cds.
ACCESSION
AF490511
VERSION
AF490511.1 GI:22023792
KEYWORDS
Canis familiaris (dog)
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 2826)
Sidiyanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
Canine CNGB3 mutations establish cone degeneration as orthologous
to the human achromatopsia locus ACHM3
Hum. Mol. Genet. 11 (16), 1823-1833 (2002)
REFERENCE
2 (bases 1 to 2826)
Sidiyanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
Direct Submission
Submitted (05-MAR-2002) Baker Institute, Cornell University,
Hungerford Hill Rd., Ithaca, NY 14853, USA
FEATURES
Location/Qualifiers
1..2826
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
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/gene="CNGB3"
25..2373
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/product="cyclic nucleotide gated channel beta subunit"
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ORIGIN						
QSIRRAALPRGTTTQSQSLIISWAPSAEAGEVLTIEUVKAKQ"						
Query Match	69.2%	Score 1682.2;	DB 4;	Length 2826;		
Beet Local Similarity	83.6%;	Pred. No. 3.9e-313;				
Matches 1972;	Conservative	0; Mismatches	312;	Indels	75;	Gaps 3;
Qy	78	GAATGAAGAAGGCTCTCACCAAGTAATACGTCTCAGCAAAACCACAGCACAGGAAGAAA	137			
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Qy	138	CAAAGGTGAGAGAAATCTCTCAAAACNAGTCAACTCCAGTCAGCTCGTAGAGCCACA	197			
Db	144	CAAAGGTGAATAAATCTCTCCAAACCAAGATCACTCCAGTCAGCTTGTAAGAAATCACA	203			
Qy	198	CACCAACATACAAGACAACACTCTCCAAGAAAAATTCCTCTGGAGATCTGCACCAAAACCC	257			
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Qy	258	TGACCCCTCAAAATGACGAGAACCAACTGGAAACAGTGCCAGAGCAGAAGGAATGGACCC	317			
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Qy	318	CGGAAAGAGGTCCAAACAGCCCACAAAACAAACCCGCTGCAGCTCTGTTATAAATGA	377			
Db	324	TGGAAAAAGAGGCCCTAGTCAGCCCCAAAAGCAAAACCCCTTGGAGTCCCTGTTATAAATGA	383			
Qy	378	GTATGCCGATGCCCGCTACACAACCTGGTGAAGAAAGTGGTCAAAAGNACAGCCCTCTA	437			
Db	384	GTATGCTGATGCTCAGCTACACACCTGGTGAGAAAGATGGTCAAGAACAATGCTCTA	443			
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Qy	498	GCCACAGCGTGTACCAACAGTAAGAAGAGGATGATAAGCCAA---CAGNACATTACTA	554			
Db	504	GCCACAGCGGTACCATCAACAGAGAGCAATGCTAAGCTAAGAGTAAGAGAAACATTACTA	563			
Qy	555	CAGGCTGTGTGGTTCAAAGTCAAAGAGATGSCCTTTAAAGAGTACTTTAAAGCCAAATTA	614			
Db	564	TCACATATTGTGTTTTAAATTCAGAAAGTGCCTCTGACAGGTACTCTAAGACGATTTAG	623			
Qy	615	ACTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTTGCTTGT	674			
Db	624	ACTTCCAGGAAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTTGCTTGT	683			
Qy	675	CACTCTTGCCTATAACTGGAACTGCTGGTTTATACCACTGGCCCTGCTCTCCCATATCA	734			
Db	684	CACCATTTGCCCTATAACTGGAACTGCTGGCTTATACCACTAGCCCTGCTCTTCCATATCA	743			
Qy	735	AACCGCAGACAACATACACTACTGGCTTATTCGGGACATCATATGTCATATCATCTACCT	794			
Db	744	AACACAGACAACACACTACTGGTTTATACAGACATCACATGTGATATCATCTACCT	803			
Qy	795	TTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGT	854			
Db	804	TTGTGATATGCTATTATCCAGCCAGACTCCAGTTTATAAAGAGGAGAGACATAATGGT	863			
Qy	855	GGATTCAAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTCAGTTGGATGTCG	914			
Db	864	GGATTCAAATGAGTTAAAGAGACACTACAGAGCTCTACAAAATTTTCAGTTGGATGTCG	923			
Qy	915	ATCAATATACCATTTGATATTTGCTACCTCTCTTTGGGTTTAAATCCAATGTTTAGAGC	974			
Db	924	GTCAATATGCCATTTGATGTTTTTAACTCTCTCTTTGGGTTTTTAAATCCAATTTTAGGAT	983			
Qy	975	AAATAGAGATGTTAAAGTACACTCTCATTTTTTTGAAATTTAACTCATCACCTAGAGCTATAAT	1034			
Db	984	GAATAGATATTGAAGTACACTCTCATTTTTTTGAAATTTTAACTCATCACCTAGAGCTATAAT	1043			
Qy	1035	GGACAAAGCATATATCTACAGAGTTATTGCAACAACTGGATCTGCTGTTTTATTCTGCA	1094			

Qy 2172 AGATAAAACAAAGAAATGAAGATAAAGGAAAGAAATCAAGATAAAGAAAG 2231
Db 2162 -----AGATAAAGAAAG 2174
Qy 2232 AGAGCCAGAGAGAGAGCCACTGGACAGACCTGGAATGTACAGCAAGTCTTATTCAGTGG 2291
Db 2175 AGAGCCATCAGAGAGAAATCTGGACAGCTCTGGAATGTAGAGCAAAATTTGATATTAGCAG 2234
Qy 2292 GGAAGAACCCACCTCAGTGTAGAGGACAGTGTATACCCAGAGGAGTCTCTGTCATCACT 2351
Db 2235 GGAATGCCAGTCCATTTAGAGGAGGAGCTTTTACCCAGAGGAGTCTCTGTCATCACT 2294
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Db 2295 CATCATCAGATGCTCTCTTCTGAGAGGCGAGGAGAGGTTCTGACAAATTTGAAGTCAA 2354
Qy 2412 AGAAAGGCTAAGCAATAA 2430
Db 2355 AGAAAGGCTAAGCAATAA 2373

RESULT 4

MMU243572
LOCUS Mus musculus mRNA for cyclic nucleotide-gated channel subunit CNG6
DEFINITION Mus musculus mRNA for cyclic nucleotide-gated channel subunit CNG6
(CNG6 gene).
ACCESSION AJ243572
VERSION AJ243572.1 GI:6851039
KEYWORDS CNG6 gene; cyclic nucleotide-gated channel; subunit CNG6.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 Gerstner,A., Zong,X., Hofmann,F. and Biel,M.
AUTHORS Molecular cloning and functional characterization of a new
TITLE Modulatory cyclic nucleotide-gated channel subunit from mouse
retina
J. Neurosci. 20 (4), 1324-1332 (2000)
MEDLINE 20130348
PubMed 10662822
REFERENCE 2 (bases 1 to 4710)
AUTHORS Gerstner,A.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) Gerstner A., Technische Universitaet
Muenchen, Pharmakologie und Toxikologie, Biedersteiner Str. 29,
D-80802 Muenchen, GERMANY
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ORIGIN

Query Match 56.1%; Score 1362.4; DB 10; Length 4710;
Best Local Similarity 76.2%; Pred. No. 8.9e-252;
Matches 1795; Conservative 0; Mismatches 496; Indels 65; Gaps 7;

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Best Local Similarity 64.3%; Pred. No. 6.9e-101;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

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DEFINITION Homo sapiens rod photoreceptor CNG-channel beta subunit (RCNC2)
ACCESSION AF042498
VERSION AF042498.1 GI:2921582
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4382)
AUTHORS Grunwald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.
TITLE Identification of a domain on the beta subunit of the rod
cGMP-gated cation channel that mediates inhibition by
calcium-calmodulin
JOURNAL J. Biol. Chem. (1998) In press
REFERENCE 2 (bases 1 to 4382)
AUTHORS Grunwald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-1998) Neuroscience, Johns Hopkins University
School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA
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ORIGIN

Query Match 23.8%; Score 577.4; DB 9; Length 4382;
Best Local Similarity 64.3%; Pred. No. 6.9e-101;
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VERSION
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source

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Best Local Similarity 64.2%; Pred. No. 1.4e-100;
Matches 865; Conservative 0; Mismatches 482; Indels 0; Gaps 0;

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SOURCE
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Klausner,R.D., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Datchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4763)
Director MGC Project.
Direct Submission
Submitted (27-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov

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 Qy 1997 TCCACACGAAGAAGACAGACACCCAAAACCTGTTTAAAACTCTCCTAGGAGGCACAGGAAA 2054
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 VERSION AF074012.1 GI:3309621
 KEYWORDS
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 ORGANISM Bos taurus
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 REFERENCE 1 (bases 1 to 3083)
 AUTHORS Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and
 Weyand,I.
 TITLE Cyclic nucleotide-gated channels on the flagellum control Ca2+
 entry into sperm
 J. Cell Biol. 142 (2), 473-484 (1998)
 MEDLINE 98345361
 PUBMED 9679145
 REFERENCE 2 (bases 1 to 3083)
 AUTHORS Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and
 Weyand,I.
 TITLE Direct Submission
 Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse,
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 Query Match 23.5%; Score 572.2; DB 4; Length 3083;
 Best Local Similarity 64.1%; Pred. No. 7.2e-100;
 Matches 862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
 Qy 617 TTCAAACAGCATAGATTTCATACACATCGACTCTATCTCTGTGGCTTGTCTGTCA 676

ORIGIN

Query Match	23.5%	Score 572.2	DB 4	Length 3083
Best Local Similarity	64.1%	pred. No. 7.2e-100		
Matches 862	Conservative 0	Mismatches 483	Indels 0	Gaps 0

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||||| 2146 CTAAGCTGTGGCCCATGCGTTTACCACTCTTCATCTGATGAAGGACCTGAATG 2205
||||| 1877 AAATCTAGTGATATCCAGATCTGAAAGATCTCTCATGAAGAAACCGAGAGTCTTT 1936
||||| 2206 AAATCTGTGATATCCGAGTCTCAGAAAGTTCCTCGCAAGAAAGCCAGGCGAATGC 2265
||||| 1937 TAAAGCAGAGGCTAAGACCCGAGA 1961
||||| 2266 TGAGAAATAACAAGCCCAAGGA 2290

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DEFINITION B.taurus mRNA for CNG4c protein.
ACCESSION X94707
VERSION X94707.1 GI:1154636
KEYWORDS CNG4c gene; CNG4c protein; cyclic nucleotide-gated cation channel; modulatory subunit.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1
Biel, M., Zong, X., Ludwig, A., Sauter, A. and Hofmann, F.
Molecular cloning and expression of the Modulatory subunit of the cyclic nucleotide-gated cation channel
J. Biol. Chem. 271 (11), 6349-6355 (1996)
96198098
8626431
2 (bases 1 to 3253)
Biel, M.
Direct Submission
Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und Toxikologie, Technische Universitaet Muenchen, 80802 Muenchen, Biedersteiner Strasse 29, FRG
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Best Local Similarity 64.1%; Pred. No. 7.1e-100;
Matches 862; Conservative 0; Mismatches 493; Indels 0; Gaps 0;
Qy 617 TTCAAACAGCATAGATTATACAGATCGACTCTATCTCTGTGGCTTTGCTGTGCA 676
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Search completed: March 27, 2005, 16:03:45
Job time : 10112 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 03:41:23 ; Search time 1203 Seconds
(without alignments)
11957.582 Million cell updates/sec

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Perfect score: 2430
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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	573.6	23.6	3811	5	AAS91658 DNA encod
6	569.6	23.4	4238	10	ADB53355 Primary r
7	568	23.4	3236	13	ADG64556 Norway ra
8	518	21.3	2244	5	AAS76156 DNA encod
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24	129	5.3	526	4	Aak36108	Aak36108 Human bon
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29	128	5.3	2877	10	ADF56507	Adf56507 Modified
30	127	5.2	127	4	ABA74393	ABA74393 Human foe
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32	127	5.2	127	4	AAK49030	AAK49030 Human bon
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ALIGNMENTS

RESULT 1.

AAD25729

ID AAD25729 standard; DNA; 2757 BP.

XX

AC AAD25729;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human cyclic nucleotide-gated cation channel 3 beta subunit DNA.

XX

KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;

KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;

KW male infertility; genetic defect; reporter-ligand interaction; CNG;

KW viral infection; cancer; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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FT CDS 112..2541

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FT /note= "This region is specifically claimed in claim 4 as

FT SEQ ID NO:4"

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FT /tag= c

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PN WO200188090-A2.

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PD 22-NOV-2001.

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PF 15-MAY-2001; 2001WO-US015814.

XX

PR 15-MAY-2000; 2000US-0204445P.

XX

PA 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX

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PT	New polypeptide, useful for screening for modulators of cyclic nucleotide-gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.	Db	772	TGGCTCTTGCTTGCTCACTCTTGCTTATACTGGAACTGCTGGTTTATACCACTCGCGCTC	831
XX	Claim 4; Fig 2; 83pp; English.	Qy	721	GTCTTCCCATATCAAAACCGAGACAACTACTCTGGCTTATTGCGGACATCATATGT	780
CC	The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vitro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is a DNA encoding CNG3B protein	Db	832	GTCTTCCCATATCAAAACCGAGACAACTACTCTGGCTTATTGCGGACATCATATGT	891
XX		Qy	781	GATATCATCTACCTTTATGATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAAAGGA	840
CC		Db	892	GATATCATCTACCTTTATGATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAAAGGA	951
XX		Qy	841	GGAGACATAATAGTGGATTCAAATGAGCTAAAGAAACACTACAGGACTTCTACAAAATTT	900
CC		Db	952	GGAGACATAATAGTGGATTCAAATGAGCTAAAGAAACACTACAGGACTTCTACAAAATTT	1011
XX		Qy	901	CAGTTGGATGTCCGATCAATAATACCATTTGATATTTGTACTCTCTTTGGTTTAAAT	960
CC		Db	1012	CAGTTGGATGTCCGATCAATAATACCATTTGATATTTGTACTCTCTTTGGTTTAAAT	1071
XX		Qy	961	CCANTGTTTAGAGCAATAGGATGTTAAAGTACACTTCACTTTTGAATTTTAAATCATAC	1020
CC		Db	1072	CCANTGTTTAGAGCAATAGGATGTTAAAGTACACTTCACTTTTGAATTTTAAATCATAC	1131
XX		Qy	1021	CTAGAGTCTATAATGGACAAAGCATATCTACAGAGTTATTTCGAACAACTCGATCTTG	1080
CC		Db	1132	CTAGAGTCTATAATGGACAAAGCATATCTACAGAGTTATTTCGAACAACTCGATCTTG	1191
XX		Qy	1081	CTGTTTATTCTGCAATTAATGCTGTGTTTATTACTTGGGCTTCAAATATGAAGAAAT	1140
CC		Db	1192	CTGTTTATTCTGCAATTAATGCTGTGTTTATTACTTGGGCTTCAAATATGAAGAAAT	1251
XX		Qy	1141	GGCACTACTAGATGGTGTATGATGGGGAAGAAAGAGTATCTGAGATGTTATTATTGG	1200
CC		Db	1252	GGCACTACTAGATGGTGTATGATGGGGAAGAAAGAGTATCTGAGATGTTATTATTGG	1311
XX		Qy	1201	GCAGTTTCGAACTTTAAATACCAATGGTGGCTTTCAGAACCAAACTTTATTGAAAT	1260
CC		Db	1312	GCAGTTTCGAACTTTAAATACCAATGGTGGCTTTCAGAACCAAACTTTATTGAAAT	1371
XX		Qy	1261	GTTTTTCAACTCTTGAAATTTTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATGGTCA	1320
CC		Db	1372	GTTTTTCAACTCTTGAAATTTTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATGGTCA	1431
XX		Qy	1321	ATGAGAGATGTCATTTGGAGCAGCTACGCCAATCAGAACTACTCCGCGCTGCATGGAT	1380
CC		Db	1432	ATGAGAGATGTCATTTGGAGCAGCTACGCCAATCAGAACTACTCCGCGCTGCATGGAT	1491
XX		Qy	1381	GACACCAATTCCTACATGAAACAAATTAATCTCAATTCCTAAACTTGTCAAAGCGAGT	1440
CC		Db	1492	GACACCAATTCCTACATGAAACAAATTAATCTCAATTCCTAAACTTGTCAAAGCGAGT	1551
XX		Qy	1441	ACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGATCTGATTTGCTTA	1500
CC		Db	1552	ACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGATCTGATTTGCTTA	1611
XX		Qy	1501	ACCCCTACCACTACCGGTCAGTTCAGCTCCGCTCCGCTTGTGAACTTCCAGCATCATC	1560
CC		Db	1612	ACCCCTACCACTACCGGTCAGTTCAGCTCCGCTCCGCTTGTGAACTTCCAGCATCATC	1671
XX		Qy	1561	AAAGTCGACTTGTTCAGAGGTTTGCATACACAGATGATTTATGACATGTTGTAAGATT	1620
CC		Db	1672	AAAGTCGACTTGTTCAGAGGTTTGCATACACAGATGATTTATGACATGTTGCTAAGATT	1731
XX		Qy	1621	AAATCCGTTCTCTATTTGCTGGTGAATTTGTCTCAAAAAAGGGAGAAATTTGGCAAG	1680
CC		Db	1732	AAATCCGTTCTCTATTTGCTGGTGAATTTGTCTCAAAAAAGGGAGAAATTTGGCAAG	1791

Query Match 100.0%; Score 2430; DB 6; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTTTAAATCGTGCACAAAGTCAACAAGTGAAGCCTATAGGAGAGAACAAATGAGAAT	60
Db	112	ATGTTTAAATCGTGCACAAAGTCAACAAGTGAAGCCTATAGGAGAGAACAAATGAGAAT	171
Qy	61	GAACAAGTTCTGTCGGATGAGAGGCTCTCACCAAGTAAATCACTGTGAGCAACC	120
Db	172	GAACAAGTTCTGTCGGATGAGAGGCTCTCACCAAGTAAATCACTGTGAGCAACC	231
Qy	121	ACAGCACAGGAAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	180
Db	232	ACAGCACAGGAAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	291
Qy	181	ACGTCTGAAGAGCCACACACCAATACAGACAACTCTCCAAAGAAATTCCTCTGGA	240
Db	292	ACGTCTGAAGAGCCACACACCAATACAGACAACTCTCCAAAGAAATTCCTCTGGA	351
Qy	241	GATCTGACCAACCTGACCTCAAAATGACAGCAACCACTGGAACAGTGCAGAG	300
Db	352	GATCTGACCAACCTGACCTCAAAATGACAGCAACCACTGGAACAGTGCAGAG	411
Qy	301	CAGAAGAAATGGACCCCGGGAAGAGGTCCAAACAGCCACAAACCAACCGCTGCA	360
Db	412	CAGAAGAAATGGACCCCGGGAAGAGGTCCAAACAGCCACAAACCAACCGCTGCA	471
Qy	361	GCTCCTGTTTAAATGAGTATGCGATGCCAGCTACAACTGCTGGTAAAGAAATGCGT	420
Db	472	GCTCCTGTTTAAATGAGTATGCGATGCCAGCTACAACTGCTGGTAAAGAAATGCGT	531
Qy	421	CAGAAGCAAGCCCTCTACAGAAAGATTTGGTAGAGGAGATCTCTCCACCCGAGCC	480
Db	532	CAGAAGCAAGCCCTCTACAGAAAGATTTGGTAGAGGAGATCTCTCCACCCGAGCC	591
Qy	481	AGCCCAACAACTCAAGCCCGCTGTACACCAAGTAAAGAAAGCGATGATAGGCA	540
Db	592	AGCCCAACAACTCAAGCCCGCTGTACACCAAGTAAAGAAAGCGATGATAGGCA	651
Qy	541	ACAGAACTTATACAGGCTGTTGGTTCAAAAGTCAAAGATGCTTTAAACAGAGTAC	600

QY 1457 CATGGAGCTCTCAAGAAGTGTAGATGAGTCTGATTGCTTAAGACCTTACCAACTACGG 1516
 Db 2825 CCTGGCACTCGCAAGGCTGTGGATGAGTCAGAGCTGATGTGAGCTTCCAGACAAGA 2884
 QY 1517 TCCAGTGTAGCCTCGCCATGATGTGAACCTCAGCATCATCAGCAAGCTGCATGTTCA 1576
 Db 2885 TCGGCTGGACTCGCCATCGAGTGAACCTCAACATCGTTAGCAAGTCGCACCTTTTC 2944
 QY 1577 AGGGTGTGTATACAGATGATTTATGACATGTTGCTAAGATTTGAAATCCCGTCTCTATT 1636
 Db 2945 AGGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTGTCTACC 3004
 QY 1637 TGCCTGTGACTTGTCTGCAAAAGGAGGAAATTTGGCAAGAAATGATATCATCAAGC 1696
 Db 3005 TGCCCAACGACTATGTGTGCAAGAGGGGAGATCGGCCGTGAGATGTACATCATCCAGG 3064
 QY 1697 ATGGAGAGTCCCAAGTCTCTGGAGCCTGATGTTGATGTTAAAGTCTGTTACTCTGAAG 1756
 Db 3065 CAGGCAAGTGAGGTCTTGGCGGCCCTGATGGGAAATCTGTGTGAGCTGAAAG 3124
 QY 1757 CTGGTCTCGGTGTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCAACTG 1816
 Db 3125 CTGGATCTGTGTTGGAGAAATAGCTTCTGCTGCTGTTGGGGCGGGAACCGGCGCAGG 3184
 QY 1817 CCAATGTGGTGGCCCAACGGTGTGCAATCTTTTAACTCTAGACAAAAGACCCCTCAAG 1876
 Db 3185 CCAACGTGGTGGCGCACGGGTTTACCAACCTCTTCTATCTGATTAAGAAGACCTGAATG 3244
 QY 1877 AAATCTAGTCATATCATGATCTGAAAGATCTTGAAGATCTTATGAGAAAGCCAGTGCTTT 1936
 Db 3245 AGATTTTGGTGATTTATCTGAGTCTCAGAAAGTTACTCCGGAAGAAAGCCAGGCGCATGC 3304
 QY 1937 TAAAGCAGAGGCTAAGACCCGAGAG 1963
 Db 3305 TGAGAGCAACAATAAGCCCAAGGNG 3331

RESULT 4

ID ABZ80565 standard; cDNA; 2607 BP.
 XX
 AC ABZ80565;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Nucleotide sequence of hbeta1b.
 XX
 KW OCN1; OCN2; beta1b; human;
 XX olfactory cyclic nucleotide gated channel subunit; ss.
 OS Homo sapiens.
 XX
 PN W02003004611-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 08-JUL-2002; 2002WO-US021184.
 XX
 PR 06-JUL-2001; 2001US-0303140P.
 PR 10-DEC-2001; 2001US-0337154P.
 XX
 PA (SENO-) SENOMYX INC.
 XX
 PI Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JB;
 PI Servant G, Callamaras N;
 XX
 DR WPI; 2003-229406/22.
 XX
 DR P-PSDB; ABR39396.
 XX
 PT Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b
 PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for
 PT identifying the CNG channel activators useful for enhancing smell.

XX

Claim 14; Page 89; 97pp; English.

The present invention relates to a nucleotide sequences encoding human OCN1, OCN2, or beta1b olfactory cyclic nucleotide gated (CNG) channel subunit, its action being an olfactory CNG channel activity modulator. A host cell which expresses human OCN1, OCN2 and/or beta1b is useful in a mammalian cell-based assay for the profiling and screening of putative modulators of a human olfactory cyclic nucleotide gated (CNG) channel. The method is used to identify a compound as one which particularly modulates CNG activity based on a detectable change in fluorescence. The test cell expresses each of the human OCN1, human OCN2 and human beta1b subunits. A fluorescence plate reader or a voltage imaging plate are used to monitor changes in fluorescence. The compounds that activate olfactory CNG channel enhance smell and can be used to make foods more palatable for individuals with attenuated olfactory function. The present sequence represents the nucleotide sequence of hOCN1

Sequence 2607 BP; 614 A; 782 C; 719 G; 492 T; 0 U; 0 Other;

Query Match 23.8%; Score 577.4; DB 8; Length 2607;
 Best Local Similarity 64.3%; Pred. No. 1.1e-116;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY 617 TTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTTGTGTGCA 676
 Db 782 TTCCCCAGAGCATTTGACCCGCTGACCAACCTGATGTATGTCTATGGCTGTCTTCGTGG 841
 QY 677 CTCTTGCTTAACTGNACTGCTGTTTATACACTGGCCTGCTTCCCATATCAA 736
 Db 842 TGATGGCTGGAATTTGAACTGTTGGCTGATTCGCGTGGCTTCCCTACCAGA 901
 QY 737 CCGCAGACAACATACATCTACTGGCTTATTCGGGACATCATATGTATATCATCTACCTTT 796
 Db 902 CCCCGACACATCCACCATCTGGCTGTGTGATTTACCTATGGACCTCATCTACTTCC 961
 QY 797 ATGATATGCTATTATTCAGCCAGACTCCAGTTTGAAGAGGAGGAGACATAATAGTGG 856
 Db 962 TGGACATCACCGTGTTCAGACACGCTGCAAGTTTGTTCAGAGGGGGGACATCATACGG 1021
 QY 857 ATTCAATAGCTAAGGAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGAT 916
 Db 1022 ACAAAGGACATCGGAAATAACTACCTGAAGTCTCGCCGCTTCAAGATGACCTGTCTCA 1081
 QY 917 CAATAATACCATTTGATATTGCTACCTCTCTTTGGGTTTAAATCCAAATGTTTAGAGCAA 976
 Db 1082 GCCTCTCGCTTGGATTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCCGCTGC 1141
 QY 977 ATAGGATGTTAAAGTACACTTCAATTTTGAATTAATATCATCTAGAGTCTATAATGG 1036
 Db 1142 CCCGCTGTTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGGCTGGAATCCATCTCA 1201
 QY 1037 ACNAGCATATATCTACAGAGTTATTCGAACAACCTGGATCTTCTGTTTATTCTGCACA 1096
 Db 1202 GCAAAGCCTACGTGTACAGGGTTCATCAGGCTTACAGGCTTACCTTCTCTACAGCTGCAAT 1261
 QY 1097 TTAATGCTGTGTTTATTATCTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGTGG 1156
 Db 1262 TGAATTCCTGTCTTATTATCTGGCATCGGCTTATCAGGGCTCGGCTCCACTCAGTGG 1321
 QY 1157 TGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTTATTATTTGGGCAAGTTCGAACTTAA 1216
 Db 1322 TTTACGATGGCTGGGAAACAGTTTATATCGCTTACTACTTTGCTGTGAAGACCTCTCA 1381
 QY 1217 TTACCATGTTGGCTTCCAGAACCAAACTTATTGAAATTTGTTTCAACTCTTGA 1276
 Db 1382 TCACCATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA 1441
 QY 1277 ATTTTCTTCTGGAGTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGTTG 1336
 Db 1442 ATATTTTCAGGGGCTCTTTGCTTTCTGTGTATGATCGGACAGATGAGAGATGTTG 1501
 QY 1337 GAGCAGCTACAGCCAATCAGAACTACTTCCGCGCTGCTGATGGATGACACCATTCCTACA 1396

QY 1180 TATCTGAGATGTTATTTATTTGGGAGTTCGAACCTTTAAATTACATTTGGTGGCCCTTCAGAA 1239
Db 2549 TATATTCGCTGTACTACTTTGCTGTGAAGACCTTCATCACATCGGGGGCTGCTGAC 2608
QY 1240 CCACAACTTTATTTGAAATTTCTTTTCAACTCTTTGAAATTTTCTTCTGGAGTTTGTG 1299
Db 2609 CCCAGACACTCTTTGAAATTTCTTTCAAGTCTGCTGAAATTTTACCGGCGCTTTGCT 2668
QY 1300 TTCTCCAGTTTAAATTTGGTCAGATGAGAGATGATTTGGAGCAGCTTACAGCCAAATCAGAAC 1359
Db 2669 TTCTCTGTGATGATCGGACAGATGAGAGATGTTGGTAGGGCGCCACCGCGGGACAGACC 2728
QY 1360 TACTTCCGGCTGATGATGACACCACTTGCCTACATGAACAATTCCTCAATTCCTTAA 1419
Db 2729 TACTACCCGAGCTGATGACAGCAGCGGTGAAGTACATGAATTTCTCAAGATTCCTCCAG 2788
QY 1420 CTTGTGCAAAAGCGAGTTTCGGACTTTGGTATGAATATATACATGGGACTCTCAAGAATGCTA 1479
Db 2789 TCCGTGAGAACCGGCTCAGACCTTGTACGAGTACACTGGCATCTCGAAGGATGCTG 2848
QY 1480 GATGATCTGATTTTCTTAAAGACCTTACCACTACCGTCCAGTTAGCCCTCGCCATTGAT 1539
Db 2849 GATGATCAGAGCTGATGTGAGCTTCCAGACAAGATCGGCTGGAACCTCGCCATCGAC 2908
QY 1540 GTGAACCTTCAGCATCATCAGCAAGTGCAGTTGTTCAAGGGTTGTGATACACAGATGAT 1599
Db 2909 GTGAACCTCAACATCGTTAGCAAGTGCAGCTCTTTTCAGGGCTGTGACCGGAGATGATC 2968
QY 1600 TATGACATTTGCTAAGATTGAATCCGTTCTCTATTTGCTGTGACTTTGCTGCAAA 1659
Db 2969 TTTGACATGCTGAAGAGGCTTCGCTCTGTTGTCTACCTGCCCAAGCATATGTGTGCAAG 3028
QY 1660 AAGGAGAAATTTGCAAGAAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTTCTTGA 1719
Db 3029 AAGGGGAGATCGGCGGTGAGATGTACATCATCCAGGAGGCAAGTGCAGTCTTGGGC 3088
QY 1720 GGCCCTGATGTACTAAAGTTCTGTTACTCTGAAAGCTGGTGGTGGTGGAGAAATC 1779
Db 3089 GGCCCTGATGGAAATCTGTGCTGTGAGCTGAAAGCTGATCTGTGTTGGAGAAATA 3148
QY 1780 AGCCTTCTAGCAGAGGAGGAGAAACCGTGCAGTCCAAATGTGTTGGTGGCCACGGGTT 1839
Db 3149 AGCTTCTGCTGTGTTGGGGGGGAGAACCGGCGCACGGCCACAGTGGTGGCGACGGGTT 3208
QY 1840 GCCAATCTTTAACTCTAGACAAAGAACCCCTTCAAGAAATCTAGTGCATTATCCAGAT 1899
Db 3209 ACCAACCTCTTCACTCTGATGAAGAGACCTGATGATGATTTGTTGCTATATCTGAG 3268
QY 1900 TCTGAAAGATCTCATGAAGAACCCAGAGTGTCTTTTAAAGCAGAAAGGCTTAAGACCGCA 1959
Db 3269 TCTCAGAAAGTTACTCCGGAAGAACCCAGGCGCATGCTGAGAAGCAACAATAAGCCCAAG 3328
QY 1960 GAAG 1963
Db 3329 GAGG 3332

RESULT 6
ADB53355
ID ADB53355 standard; DNA; 4238 BP.
XX AC ADB53355;
XX AC
XX AC
DT 04-DEC-2003 (first entry)
XX DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3997.
XX DE
XX DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX DE toxicity marker; toxicity progression; drug screening;
XX DE primary rat hepatocyte toxicity modelling; gene; ds.
XX OS
XX OS Rattus norvegicus.

PN WO2003065993-A2.
XX 14-AUG-2003.
XX 04-FEB-2003; 2003WO-US003482.
XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374113P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX (GENE-) GENE LOGIC INC.
XX Mendrick D; Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of tox mean and non-tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3897; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the tox mean and non-tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 4238 BP; 1129 A; 1107 C; 1313 G; 689 T; 0 U; 0 Other;
Query Match 23.4%; Score 569.6; DB 10; Length 4238;
Best Local Similarity 64.6%; Pred. No. 67e-115;
Matches 848; Conservative 0; Mismatches 464; Indels 0; Gaps 0;
QY 617 TTCCAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGGCTCTTGTGTGCA 676
Db 2277 TCCCCCAGAGCATCGACCCACTGACCAACCTCATGTATCATCTCTGGCTGTTCTCGTGG 2336
QY 677 CTCTTGGCTATACTGGAACCTGCTGTTTATACACCTGGCGCTCGTCTCCCATATCAA 736
Db 2337 TGCTGGCTGGAACCTGGAACCTGCTGCTGATTCCTGTGCGCTGGCGCTTCCCGTACCAGC 2396
QY 737 CCGCAGACAACATACACTACTCTGGCTTATTCGGGACATCATATGTATCATCTACCTTT 796
Db 2397 GGGCAGACAACATCACTCTGGCTGCTCATGTGACTACTGTGCGACTTATCATCTACCTCC 2456
QY 797 ATGATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGG 856

Db	2457	TGGACATCAACGGTGTCCAGATGGCTCTCCAGTTTGTCAAAGGCGGGACATCATACAG	2516
Qy	857	ATTCAATGAGCTAAGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTGCGAT	916
Db	2517	ATAAGAGGAGATGCGTAATAATTACCTGAAGTCTCAACGATTTAAGATGGACTTGCTCT	2576
Qy	917	CAATAATACCAATTGATATTGCTTACCTCTCTTTGGGTTTAATCCAATGTTAGAGCAA	976
Db	2577	GCCTTTTGCCTTTGGATTCTCTACTTGAAACTTGGCGTGAACCCCTCTTCGCGCTGC	2636
Qy	977	ATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACCTAGAGTCTATAATGG	1036
Db	2637	CCGCTCGCTGAAGTACATGGCTTCTTTGAGTTTAATAACCGTCTGAAGGCCATCTCA	2696
Qy	1037	ACAAAGCATATCTACAGAGTTATTCGAACAACCTGGATACTTGTGTTTATTCTGCACA	1096
Db	2697	GCAAAGCCTACGTTTACAGGGTTATCAGAGGTTATCAGGACCAACCGCTTACCTGCTGTATAGCTTGCATC	2756
Qy	1097	TTAATGCTGTGTTTATTACTGGCTTCAAACTATGAAGAAATTGGCACTACTAGATGGG	1156
Db	2757	TCAACTCTGTTTACTTGGCGTTCGGCTTCCAGGCGATCGGTTCCACTCACTGGG	2816
Qy	1157	TGTATGATGGGAGGAAACGAGTATCTGAGATGTTATTATGGGCAAGTTTCAACTTTAA	1216
Db	2817	TTTATGACGGCGTGGGAAACAGCTTACATTCGATGCTACTACTGGCTGTGAAAACCTCA	2876
Qy	1217	TTACCATTGTGGCTTCCAGAACCAAACTTTATTGAAATGTTTTCAACTCTTGA	1276
Db	2877	TCACCATCGGAGGACTGCCCGACCCCGACAGCGCTCTTTGAGATCGTCTCCAGCTGCTGA	2936
Qy	1277	ATTTTTTTCTGGAGTTTTGTGTTCTCCAGTTTAATTGTCAGATGAGAGATGTGATTG	1336
Db	2937	ATTATTTTACAGTGCTTCGCTTCTCTGTGATGATGGACAGATGAGAGATGTGTGG	2996
Qy	1337	GAGCAGCTACAGCCAATCAGAACTACTTCCGCGCTGTCATGATGACACCATTTGCCCTACA	1396
Db	2997	GGCGCGCACGGCAGCGACAGCTACTACCGAGCTGCATGGACAGCAGCGTGAAGTACA	3056
Qy	1397	TGAACAATTAATCTCATCTTAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA	1456
Db	3057	TGAATCTTCTAAGATCCCCAGGCTGTGTGCAAGAACCGGCTCAAGACCTGGTGTACGAATACA	3116
Qy	1457	CATGGGACTCTCAAGAACTCTAGATGAGTCTGATTTGCTTAAGACCCCTACCAACTACGG	1516
Db	3117	CTTGGCACTCAAGAGCATGCTGATGAGTCAAGCTGATGGTTTCAGCTTCCGGAACAGA	3176
Qy	1517	TCCAGTTAGCCCTCGCCATTGATGTGAATCTTACGATCATCAAGAAAGTTCGACTTGTTC	1576
Db	3177	TGCGTCTGGACCTGGCCATTGACGTAAACTACAACATTTGTCAAGAAAGTGGCGCTCTTCC	3236
Qy	1577	AGSGTTGTGATACACAGATGATTTATGACATGTTGTCTAAGATTGAATTCGTTCTCTATT	1636
Db	3237	AGGGCTGCGACCGGACGATGATCTTCGACATGCTCAAGCGACTTCGCTCAGTCTGTACC	3296
Qy	1637	TGCTGTGTGATTTGTCTGCAAAAGGAGAAATTTGCAAGGAAATGTATATCATCAAGC	1696
Db	3297	TACCCATGACTATGTGTGCAAGAGGGGAGATTTGGCCGAGAGATGTATATTATCCAGG	3356
Qy	1697	ATGGAGAAGTCCAAGTTCTTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAG	1756
Db	3357	CGGGGACAGGTGCAGGTGCTGGCGGCCACAGATGMAAGGCTGTCTCTGTGACACTCAAAG	3416
Qy	1757	CTGGGTGCGTGTGTGGAGAAATCAGCCTTCTACGACGAGGAGGAGAAACCGTTCGAACTG	1816
Db	3417	CCGGATCGGTTTGTGGAGATGAAGCTTGTGCTGTCTGGGGCGGTAACAGGCGCACGG	3476
Qy	1817	CCAATGTGGTGGCCACGGGTTTGCCTCTTTTAACTCTAGACAAAAGACCCCTCCAAG	1876
Db	3477	CCAAATGTGGTGGCCACGGCTTCAACCAATCTCTTCAATCTGGATTAAGAGGACTTGAATG	3536
Qy	1877	AAATCTTAGTGCATTTATCCAGATTTCTGAAAGGATTCCTCATGAAAGAGCCAG	1928

3537

AGATTTTGGTGCATTACCTGAATCTCAGAAGCTGCTCGGAAGAGGCCAG

3588

RESULT 7

AD564556

ID

ADS64556 standard; DNA; 3236 BP.

XX

AC

ADS64556;

XX

DT

16-DEC-2004 (first entry)

XX

DE

Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA.

XX

KW

cyclic nucleotide concentration; screening;

KW

cyclic nucleotide-gated ion channel 4.3; CNG4.3; ds.

XX

OS

Rattus norvegicus.

XX

PN

W02004083803-A2.

XX

PN

30-SEP-2004.

XX

PF

06-MAR-2004; 2004WO-BP002317.

XX

PR

18-MAR-2003; 2003DE-01011769.

XX

PA

(FARB) BAYER HEALTHCARE AG.

XX

PI

Wunder F;

XX

PI

WPI; 2004-728498/71.

XX

DR

Determining intracellular concentration of cyclic nucleotides, useful for identifying, e.g. receptor ligands and enzyme inhibitors, comprises using cells that express a cyclic nucleotide activated ion channel and a photoprotein.

XX

PS

Example; SEQ ID NO 2; 20pp; German.

XX

CC

The invention relates to a novel method for determining the intracellular concentration of cyclic nucleotides. The method comprises preparing a cell that expresses a CNG (cyclic nucleotide-activated) ion channel together with a photoprotein and detecting the intracellular concentration of cyclic nucleotides from the luminescent signal of the photoprotein. The method may be used to screen for receptor ligands and modulators of phosphodiesterase, guanylate cyclase or nitric oxide synthase, which would be potentially useful as pharmaceuticals. The method is suitable for high throughput screening, does not require radioactive tracers, has a high signal-to-noise ratio, is very quick, highly sensitive and inexpensive. The current sequence is that of the Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA of the invention.

XX

SQ

Sequence 3236 BP; 780 A; 962 C; 903 G; 591 T; 0 U; 0 Other;

Query Match

23.4%; Score 568; DB 13; Length 3236;

Best Local Similarity

64.6%; Pred. No. 1.4e-114;

Matches

847; Conservative 0; Mismatches 465; Indels 0; Gaps 0;

QY

617

TTCCAAACAGCATAGATTTCATACAGATTCGACTCTATCTCTGTGGCTTCTTGGTGTCA

676

Db

1211

TCCCCCAGAGCATGACCCACTGACCACTCATGTATACATCTGTGGCTGTCTTCGTGG

1270

QY

677

CTCTTGGCTATTAACCTGGAACCTGCTGTTATACCACTGGCTGCTTCCCATATCAAA

736

Db

1271

TGCTGGCTTGGAACTGGAACCTGCTGGCTGATTTCTGTGGCTTCCCGTACCAGC

1330

QY

737

CGCGACAGAACATACACTACTGGCTTATTCGCGCATCATATGTATATCATCTACTCTT

796

Db

1331

GGCGACAGAACATCAACCTCTGGCTGCTCATGGAATCTTGTGGCACTTCACTACTCC

1390

QY

797

ATGATATGCTATTATTCAGCCCACTCCAGTCTTGTAAAGAGGAGACATAATAGTGG

856

Db 1391 TGGACATCACCGTGTTCAGATGCGTCTCCAGTGTTCAGATGTTGTCAAGCGGGGACATCATTAACAG 1450
Qy 857 ATTCAAATGAGCTAAGAGAAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTCGCAT 916
Db 1451 ATAAGAGGAGATGCGTAATAATTAACCTGAAGTCTCAACGATTTAAGATGGATGCTCT 1510
Qy 917 CAATTAATACCAATTTGATATTTGCTACCTCTCTTTGGGGTTTAATCCAATGTTTAGAGCAA 976
Db 1511 GCCTTTGGCTTTGGATTTTCTCTACTTGAACACTTGGGGTGAACCCCTCTCTTCGCTGC 1570
Qy 977 ATAGGATGTTAAAGTACACTCTCATTTTGTGAATTTAATCATCACCTAGAGTCTATAATGG 1036
Db 1571 CCCGCTGCTGAAGTACATGGCTTCTTTAGTTTTAATAACCGTCTGAAGCCACTCTCA 1630
Qy 1037 ACAAGCATATATCTACAGAGTTAATCGAACAACTGGATCTTGTCTTTAATTTCTGCACA 1096
Db 1631 GCAAGCCTACGTTTACAGGGTTATCAGGACCCGCTACCTGCTGTATAGCTTGCATC 1690
Qy 1097 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1156
Db 1691 TCAACTCTCTGTTTACTACTGGGCTGGGCTTCCAGGGCATCGGTTCCACTCACTGG 1750
Qy 1157 TGTATGATGGGGAAGGAACGAGTATCTGAGATGTTATTTGGCAGTTCGAACCTTAA 1216
Db 1751 TTTATGACGGGTGGGGAACAGTACATTCGATGCTACTTGGGCTGTGAACCTCTCA 1810
Qy 1217 TTACCAATTTGCTGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTCAACTCTTGA 1276
Db 1811 TCACCATCGGAGGACTGCGGACCCGAGACGCTCTTTGAGATCGTCTTCAGCTGCTGA 1870
Qy 1277 ATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGTTG 1336
Db 1871 ATTTATTTTACAGGTGCTTCTGCTTCTGATGATTTGGACAGATGAGATGTTGGTGG 1930
Qy 1337 GAGCAGCTACAGCAATCAGAACTACTTCCGCTGATGATGATGATGATGATGATGATGATG 1396
Db 1931 GGGCGCCAGCGGAGGAGAGTACTACCGGCTGATGATGATGATGATGATGATGATGATG 1990
Qy 1397 TGAACAAATTAATCTTCAATCTTCAAACTTTGCAAAAGCGAGTTCCGAGCTTGGTATGAATATA 1456
Db 1991 TGAATCTTACAGATCCCGAGTCTGTGAGAACCGGCTCAAGACCTGGTATGATGATATA 2050
Qy 1457 CATGGGACTCTAAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1516
Db 2051 CTTGGCAATCAAGGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2110
Qy 1517 TCCAGTTAGCCTCGCCATTTGATGAACTTTCAGATCATCAGCAAACTGCACTGTTTCA 1576
Db 2111 TGGCTGCGACCTGGCCATTTGACGTAACGTAACATTTGTCAGCAAGTGGCGCTCTTCC 2170
Qy 1577 AGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCCGTCTCTATT 1636
Db 2171 AGGGCTGGACCGGAGATGATTTCTGACATGCTCAAGCGACTTCGCTCAGTCTGCTTACC 2230
Qy 1637 TGCCTGTGATTTTGTCTGCAAAAAGGAGAAATTTGGCAAGAAATGATATATCATCAAGC 1696
Db 2231 TACCAATGATATGTGTGCAAGAGGGGAGATTGGCCGAGAGATGATATATATATCCAGG 2290
Qy 1697 ATGAGAGATCCAAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATG 1756
Db 2291 CGGGGCGAGGTGCAAGTGTGGGCGCCAGATGGAAGGCTGTCTCTGTGACACTCAAG 2350
Qy 1757 CTGGGTGCGTGTGAGAAATCAGCCTTTCTAGCAGCAGGAGGAGGAAACCGTCTGAATCTG 1816
Db 2351 CCGGATCGGTGTTTGGAGAGATAGCTTGTCTGCTGTCTGGGGCGGTGAACAGGCGCAGG 2410
Qy 1817 CCAATGTGGTGGCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCTCTCCAAAG 1876
Db 2411 CCAATGTGGTGGCCACGGGTTTCCCAATCTCTTCAATCTCTGATGAAGAGGACTTGAATG 2470
Qy 1877 AAATTTAGTGCATTTATCAGATTTCTGAAGGATCTCTCATGAAGAACCCAG 1928
Db 2471 AGATTTTGGTGCATTTACCTTGAATCTCAGAACTGCTCCGGAAGAGGCCAG 2522

RESULT 8

AAS76156
ID AAS76156 standard; cDNA; 2244 BP.

XX AAS76156;

AC AAS76156;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #11960.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG11969.

XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

PT Claim 1; SEQ ID NO 11960; 103pp; English.

PS The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2244 BP; 720 A; 469 C; 592 G; 463 T; 0 U; 0 Other;

Query Match 21.3%; Score 518; DB 5; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1.2e-103;
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 287 GAACAGTCCAGACGACAGAGAAATGGACCCCGGAAAGAGGTCCAAACAGCCACAAA 346

Db 83 GCAAACTATCAAGGACAGAAACCAACACCCCATGTCTTCAACACAGCCACAAA 142

Qy 347 ACAACCGCCTGCAGCTCTCTTTATAAATGAGTATGCCGATGCCAGCTACACACCTGG 406

Db 143 ACAAACCGCTGACGCTCTGTTATAAATGAGTATGCGGATGCCAGCTACACAACTGG 202
Qy 407 TGAAGAAGTGCCTCAAGACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 466
Db 203 TGAAGAAGTGCCTCAAGACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 262
Qy 467 CCTCACCAGGAGCCAGCCCAAACTGAAAGCCCGCTGTACACACAGTAGTCAAAAGAAA 526
Db 263 CCTCACCAGGAGCCAGCCCAAACTGCAAGCCCGCTGTACACACAGTAGTCAAAAGAAA 322
Qy 527 GCGATGATAAGCCCAAGAACATTAACAGGCTGTGTGGTTCAAAGTCAAAAAGATGC 586
Db 323 GCGATGATAAGCCCAAGAACATTAACAGGCTGTGTGGTTCAAAGTCAAAAAGATGC 382
Qy 587 CTTTAAACAGAGTACTTAAAGGGAATTAACCTTCAACACAGCATAGATTCATACAGATC 646
Db 383 CTTTAAACAGAGTACTTAAAGGGAATTAACCTTCAACACAGCATAGATTCATACAGATC 442
Qy 647 GACTCTATCTCCGTGGCTCTTGTGCTGCTCACTCTTGGCTATACTGGAACCTGCTGTTTA 706
Db 443 GACTCTATCTCCGTGGCTCTTGTGCTGCTCACTCTTGGCTATACTGGAACCTGCTGTTTA 502
Qy 707 TACACATGCGCCTGCTCTTCCCATATCAAAACCGCAGACAAACATCACTACTGCTTATTG 766
Db 503 TACACATGCGCCTGCTCTTCCCATATCAAAACCGCAGACAAACATCACTACTGCTTATTG 562
Qy 767 CGGACATCATATGATATCATCTACCTTTTATGATGCTATTTATCCAGCCAGACTCC 826
Db 563 CGGACATCATATGATATCATCTACCTTTTATGATGCTATTTATCCAGCCAGACTCC 622
Qy 827 AGTTTGTAGAGGAGGAGACATAATA 852
Db 623 AGTTTGTAGAGGAGGAGACATAATA 648

RESULT 9

AA576184/c
ID AA576184 standard; cDNA; 2244 BP.
XX
AC AA576184;
XX
XX
DT 13-FEB-2002 (first entry)
XX
XX
DE DNA encoding novel human diagnostic protein #11988.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG11997.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity.
PS Claim 1; SEQ ID NO 11988; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2244 BP; 463 A; 592 C; 469 G; 720 T; 0 U; 0 Other;
Query Match 21.3%; Score 518; DB 5; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1-2e-103;
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 287 GAACAGTGCAGAGCAAGAAATGGACCCCGGAAAGAGGTCCAAACAGCCCAAA 346
Db 2162 GCAAACTATCAGAGGAGAGAAACCAACACCGCATGTCTCACACAAACAGCCCAAA 2103
Qy 347 ACAACCGCTCGAGCTCCTGTATTAATGAGTATGCGATGCCAGCTACCAACCTGG 406
Db 2102 ACAACCGCTCGAGCTCCTGTATTAATGAGTATGCGATGCCAGCTACCAACCTGG 2043
Qy 407 TGAAGAAGTGCCTCAAGAACAGCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCT 466
Db 2042 TGAAGAAGTGCCTCAAGAACAGCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCT 1983
Qy 467 CTTACCCGAAAGCCAGCCCAAACTGCAAGGCCCAACCGCTGTACCAACAGTAAAGAAA 526
Db 1982 CTTACCCGAAAGCCAGCCCAAACTGCAAGGCCCAACCGCTGTACCAACAGTAAAGAAA 1923
Qy 527 GCGATGATAAGCCCAAGAACATTAACAGGCTGTGTGGTTCAAAGTCAAAAGATGC 586
Db 1922 GCGATGATAAGCCCAAGAACATTAACAGGCTGTGTGGTTCAAAGTCAAAAGATGC 1863
Qy 587 CTTTAAACAGAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 646
Db 1862 CTTTAAACAGAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 1803
Qy 647 GACTCTATCTCCTGTGGCTCTTGTGCTCACTCTTGGCTTATTAACCTGGAACTGCTGTTTA 706
Db 1802 GACTCTATCTCCTGTGGCTCTTGTGCTCACTCTTGGCTTATTAACCTGGAACTGCTGTTTA 1743
Qy 707 TACCACTGCGCTCGCTCTTCCCATATCAACCGCAGACAAACATACACTACTGCTTATTG 766
Db 1742 TACCACTGCGCTCGCTCTTCCCATATCAACCGCAGACAAACATACACTACTGCTTATTG 1683
Qy 767 CGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCC 826
Db 1682 CGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCC 1623
Qy 827 AGTTTGTAGAGGAGGAGACATAATA 852
Db 1622 AGTTTGTAGAGGAGGAGACATAATA 1597

RESULT 10

ABL19457
ID ABL19457 standard; DNA; 3275 BP.

XX ABL19457;
AC 26-MAR-2002 (first entry)
DT Drosophila melanogaster genomic polynucleotide SEQ ID NO 9844.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.
PD 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PBE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX Claim 1; SEQ ID NO 9844; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC ABBS72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3275 BP; 843 A; 849 C; 873 G; 710 T; 0 U; 0 Other;
Query Match 9.2%; Score 223; DB 4; Length 3275;
Best Local Similarity 48.7%; Pred.No. 9.4e-39;
Matches 635; Conservative 0; Mismatches 665; Indels 3; Gaps 1;
Qy 650 TCTATCTCTGGGCTCTTGGTCTTGTCTCACTCTTGCCTATAACTGGAACTGCTGGTTATAC 709
Db 1552 TCTACATCTCTGGCTATGCGTGTGTATCGCTATCGTTTCTTATAACGCTTGGTATCC 1611
Qy 710 CACTGCGCTCTCTTCCCATATCAACCCGAGAACACATACATCACTTACCTTATTCGGG 769
Db 1612 CGCTGCGCTCTGTTCCCTTTCAACCAAGGAGAACACCAATATCTGCTGGCTGCG 1671
Qy 770 ACATCATATGTATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGT 829
Db 1672 ACTTTGCGCTGACATCATATATCTACTGATGTGTCTCTTTAAACATCGGGTATGT 1731
Qy 830 TTGTAAGAGGAGGAGACATAATAGTGGATTCAATGAGCTAAGGAAACACATACAGGACTT 889
Db 1732 ACCTTTTGGAGGATCTGGGTGAAACACAGAACCTCACCAGAAAGAACTACATCGGAA 1791
Qy 890 CTACAAATTTTCACTGGATTCGCATCAATAATACCAATTTGATATTTGCTACCTTCTCT 949
Db 1792 AACTGCAGTTTAAAGCTGATCTGCGCCCTCTTCCGCTGGAGCTATTTACTTTAAAC 1851
Qy 950 TTGGTTTAAATCCAAAT---GTTTATAGCAATATAGGATGTTAAAGTACACTTCAATTTT 1006
Db 1852 TCGGAACACAGCGGCTTTGGTTGCGTTTTTCCAAAGGTTCTTTAAAGATTTCAGAGCTTCTGG 1911

RESULT 11

ADD93243

ID ADD93243 standard; cDNA; 2500 BP.

XX ADD93243;

XX 29-JAN-2004 (first entry)

Qy 1007 AATTAAATCATCACTAGAGTCTATATATGGAACAAAGCATATATCTACAGAGTTATTCGAA 1066
Db 1912 AAGTGTTCGCTTTTGGATCGAGTCATATCTTCTCCGCACTTTTTCGAGTGGCAAAA 1971
Qy 1067 CAATCGGATACCTGCTGTTTATCTGGACATTAATGCTGTTGTTTATTTACTGGGCTTCAA 1126
Db 1972 CCCTAACCTACATGCTCTACATGATCCACATCAGCGGCTGCTGTACTACGCTATATGTG 2031
Qy 1127 ACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGGAAGAAACAGATATCTGA 1186
Db 2032 ACTACCGAGTCTGGACAGAACTGTTGGGTCTTCAGCGGCANAGGGCATCCCTATGTAA 2091
Qy 1187 GATGTTATTTGGGAGTTCGAACTTTTAATTAATTAATGATGGGCTTCCAGAACCAAAA 1246
Db 2092 GGTGCTTTGCTTTTCCCAACCAAGACGCGCACTTCGATAGGAAAAAACCCCAAGCGGAAC 2151
Qy 1247 CTTTATTTGAAATTTGTTTCAACTCTTGAATTTTTTTCTGGAGTTTCTGTTCTTCCA 1306
Db 2152 GTCAGGAGATGATGCTCTTCAATGACGGTGGCTGGCTAATGGGCTCTTTGTGTTGCTC 2211
Qy 1307 GTTTAAATTTGGTCAGATGAGATGATGATGGAGCAGCTTACAGCAATCAGAACTACTTCC 1366
Db 2212 TGCTTATCGTTCAGATCAGGATATCATCTCGACAGCCACTCGGATTAAGCATGATATC 2271
Qy 1367 GCGCTCGATGGATGACACCAATTCCTACATGAACAATTTACTCCATTCTTAACTTTGTC 1426
Db 2272 GCCAGCTGGAGATGAGACACTGAGTACATGCGACGCTCAATCTCTCGCAGGAGTGC 2331
Qy 1427 AAAAGCAGTTCGAGCTTGGTATGAATATACATGGACTCTCAAGAAATGCTAGATGAGT 1486
Db 2332 AGTCAGGGTCAAAATGTGGTTCCAGTTTACATGGGAGCAGCAGCGCACTTTGGATGAAT 2391
Qy 1487 CTGATTTGCTTAAAGACCTTACCAACTCGGTCCAGTTAGCCCTCGCCATGATGTGAAT 1546
Db 2392 CCAACATATTGGATGCTTTGCGCATCAATTTGAAACCGGATATCCCATCTCCGTGCA 2451
Qy 1547 TCAGCATCATCAGCAAAAGTCGACTTTTCAAGGGTTGTGATACACAGATGATTTATGACA 1606
Db 2452 TCCAAACGCTCTCCAAGGTGCAACTCTTTGCTGATTCGAGAGGCTTTACTCAGAGATC 2511
Qy 1607 TGTGCTAAGATTGAATTCGTTCTCTATTTGCTGCTGAGCTTTGTCTGCAAAAAGGAG 1666
Db 2512 TGGTTCTAAAACCTAAGGCGAGTCACATTTTTCAGGAGATTTCTGTTTCGCGCAAGCG 2571
Qy 1667 AAATTTGCAAGAAATGTATATCATCAAGCATGAGAAGTCCAAAGTTCTTGGAGCCCTG 1726
Db 2572 AAGTGGCAGAGATGATATATCTGTAACCTGGGACAGGTTCAAGTATGATGGTGTCTTA 2631
Qy 1727 ATGTTACTTAAAGTTCTGCTTACTCTGAAAGCTGGGTGCTGTTTGGAGAAATCAGCTTC 1786
Db 2632 GTAGCGATGTAGTCTGGCACTCTAACCGAAGGTTCCGTGTTCCGGGAGATCAGTCTGC 2691
Qy 1787 TAGCAGCAGGAGGAGGAAACCGTCAACTGCGAATGTTGGTGGGCCACCGGTTTGGCAATC 1846
Db 2692 TGGGAATAAATGAGCGCGATCGCAGAAACAGCAGATGTCGATCCAAAGGCTACTCCAAAC 2751
Qy 1847 TTTTAACTCTAGACAAAGAACCCCTCCAAGAAATTTCTAGTGCATTTATCCAGATTTCTGAA 1906
Db 2752 TGTTCGTGCTGCCAAATTCGGAATTTAAACGAGGTCATTTGCCCTACTATCCCAAGGCCAG 2811
Qy 1907 GGATCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAAGGC 1949
Db 2812 CGATTTCTCAAAAGCGTCTGCTCAGCTAATGCCGAAAAAATGC 2854

XX	Cyclic nucleotide gated channel alpha 1 coding sequence.
DE	ss; gene; cyclic nucleotide gated channel alpha 1 ;
XX	central nervous system; CNS; eye; blood-brain barrier;
KW	blood-retina barrier; angiogenesis ; revascularisation;
KW	retinal pigment epithelium; RPE; neurosensory retina ; choroidea ;
KW	age-related macular degeneration; AMD; diabetic retinopathy;
KW	Alzheimer's disease; Parkinson's disease; depression; bipolar disorder;
KW	schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse;
KW	anxiety; chronic pain; retinal blastoma; primary retinal detachment .
XX	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	25..2097
FT	/*tag= a
FT	/product= "Cyclic nucleotide gated channel alpha 1"
XX	WO2003087368-A2.
XX	
PD	23-OCT-2003.
XX	
XX	16-APR-2003; 2003WO-EP004003.
XX	
PR	18-APR-2002; 2002EP-00008761.
PR	05-DEC-2002; 2002US-0431173P.
XX	
PA	(LYNK-) LYNKEUS BIO TECH GMBH.
XX	
PI	Drumm K, Schloer SH, Goehring F;
XX	
DR	WPI; 2003-845328/78.
DR	P-PSDB; ADD93244.
XX	
PT	Treating central nervous system and/or eye disorders comprises
PT	administering to a subject a composition comprising a compound that
PT	modulates a target gene or gene product, outside the blood-brain and/or
PT	blood-retina barriers.
XX	
PS	Claim 19; SEQ ID NO 1; 91pp; English.
XX	
CC	This sequence encodes the human cyclic nucleotide gated channel alpha 1
CC	protein. This cDNA may be targeted in the method of the invention for
CC	treating a disorder of the central nervous system (CNS) and/or the eye.
CC	The method comprises administering to a subject a composition comprising
CC	a compound capable of modulating a target gene or gene product in a
CC	therapeutic amount, where the composition is administered outside the
CC	blood-brain and/or the blood-retina barriers. The composition is in a
CC	designed form to be introduced into the cells or tissue of the CNS or eye
CC	by a suitable carrier, characterized by the application occurring outside
CC	the blood-brain or blood-retina barriers. It is also designed for
CC	systemic administration or for administration by iontophoresis, or for
CC	retrobulbar application or as eye drops. The compound, nucleic acid
CC	molecule or vector is useful for the preparation of a composition for
CC	treating, preventing and/or delaying a disorder of the CNS and/or the
CC	eye, e.g. related to angiogenesis and/or neovascularisation, retinal
CC	pigment epithelium (RPE), neurosensory retina and/or choroidea and wet
CC	age-related macular degeneration (AMD) or diabetic retinopathy. The
CC	compound may also be used as a lead compound in drug discovery and
CC	preparation of drugs or prodrugs. The nucleic acid molecule and
CC	polypeptide are also used for the validation of test substances, lead
CC	compounds, drugs and prodrugs for the treatment of the disorder mentioned
CC	above or for the identification and isolation of downstream genes, which
CC	respond to modulation of a gene comprising the nucleic acid molecule or
CC	its encoded gene product. The method is used for diagnosing, preventing
CC	or treating the disorder cited above, which may include Alzheimer's
CC	disease, Parkinson's disease, depression, bipolar disorder,
CC	schizophrenia, amnesia, headache, stroke, insomnia, alcohol abuse,
CC	anxiety, chronic pain, retinal blastoma, primary retinal detachment or
CC	age-related macular degeneration.
XX	
SQ	Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;

Query Match	7.3%;	Score 176.4;	DB 10;	Length 2500;
Best Local Similarity	49.6%;	Pred. No. 1.5e-28;		
Matches 617;	Conservative	0;	Mismatches 591;	Indels 36;
Gaps				5;
QY	740	CAGACAAACATACACTACTGGCTATTGGCGACATCATATGTGATATCATCTACCTTTATG		799
Db	605	CTGATTACCTAGATAATTGGCTCATTTTGGATTACGTATCAGACATAGTCTATTAAATCG		664
QY	800	ATATGCTATTATCCAGCCAGACTCCACTTTTGTAGAGGAGGAGACATAATAGTGAATT		859
Db	665	ATATG---TTGTACGAACAAGGACAGGTTACCTAGAACAGGACTGCTGGTAAAGGAAG		721
QY	860	CAAAATGAGCTAAGGAAACACTACAGGACTTTTACAAAAATTTAGTTGGATGTGCGATCAA		919
Db	722	AACCTAAACCTCATATAATAATAATCAACTTGCATTTAAACTTGTATGTTCTGTCTAC		781
QY	920	TAAATACATTGATATTTGCTACTCTCTTTTGGGGTTTA---ATCCAAATGTTTAGAGCAA		976
Db	782	TGATACCAACTGATTTGCTGTATTTTAACTTAGGGTGGAACTATCCAGAAATTTAGATTAA		841
QY	977	ATAGGATGTTAAAGTACACTTCATTTTGAATTTTAATCATCATCAGCTAGAGTCTATATGG		1036
Db	842	ACAGGTTGTTACGGTTCTCTCGTATGTTTGAGTTCTTCCAGAGAACAGAAACAAGGACAA		901
QY	1037	ACAAAGCATATATCTACAGAGTTATTCGAAACAACTGGATACTTGCTGTTTATTTCTGCACA		1096
Db	902	ACTATCCAAACATCTTCAGGATTTCCAACTTGTATGTATATCGTCATCATTTATCCACT		961
QY	1097	TTAATGCCCTGTGTTTATTAATACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGG		1156
Db	962	GGAAATGCATGTGTGTTCTACTCTATTTCTAAAGCTATTGGAATTTGGAATGATACATGG		1021
QY	1157	TGTA-----TGATGGGAAGAAACGAGTATCTGAGATGTT		1192
Db	1022	CTACCTGATATTAATGATCTCGAATTTGGCGTTTGGCTAGAAATACGTATACAGCC		1081
QY	1193	ATTATTTGGGCAGTTCGAACTTTAAATTTACCAATTTGGTGGCTTCCAGAACCACTTTAT		1252
Db	1082	TTTACTGGTCTACACTGACTTTGACTTACCATTTGGTGAACACCCCTCCGCGAGGATTT		1141
QY	1253	TTGAAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTCTGGTGTGTTTCTCCAGTTTAA		1312
Db	1142	CTGAGTATGTTCTTTGGTGGTGGTGTGATTTCTCTAAATTTGGAGTGTAAATTTTGTCTAC		1201
QY	1313	TTGGTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCATCAGAACTACTTCCGGCCT		1372
Db	1202	TTGGTAAACATAGGTTCTATGATTTCCAAATGAATGCAGCAGAGCAGAAATTTCAAGCAA		1261
QY	1373	GCATGGATGACACCACTTGCTCATGAACAATTTACTTCCATTTCTTAAACTTTGTCAAAAGC		1432
Db	1262	GAAATGATGCTATCAAGCAATATATGCAATTTTCCAAATGTAGCAAGATATCGAAAGA		1321
QY	1433	GAGTTCGGAATTTGTTAATATATACATGGGACTCTCAAGAAATGCTAGATGATCTGATTT		1492
Db	1322	GGGTTATTAAATGGTTTGACTACTCTGTGGAACAAACAAAAACAGTTGATGAGAAAGAAG		1381
QY	1493	TGCTTAAGACCTTACCAACTACGGTCCAGTTAGCCCTCCCACTTGTATGATGAACTTCAGCA		1552
Db	1382	CTCTAAAGTATCTACCTGATAAACTAAGAGCAGAAATTCGCATCAACGTTCTACTTAGACA		1441
QY	1553	TCATCAGCAAAAGTCGACTTTGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTC		1612
Db	1442	CATTAAAAAGGTACGCAATTTTGTGATTTGTGAAGCTGGTCTGTTGTTGGTGTGGTCT		1501
QY	1613	TAAGATTGAAATCCGGTCTCTATTTTCCCTGGTGACTTTGTCTGCAAAAAAGGGAATAATG		1672
Db	1502	TGAAATTGCAACCCCAAGTCTACAGTCTCTGGAGATTTATTTTTCAGAAAGAAAGGGGATATCG		1561
QY	1673	GCNAGGAATGTATATCATCAAGCATGGAGAGATCCAAAGTTCTTGGAGGCCCTGATGGTA		1732
Db	1562	GACGAGAGATGTACATTATCAAGGAAGCAAACTCGCTGTGGTGGCAGATGATGGAGTCA		1621

QY 1733 CTAAAGTTCTGGT-----TACTCTGAAGAGTGGGTGGGTGGGAGAAATC--AGCCTTC 1786
DB 1622 CTCAGTTTGTGATTTGAAGCGATGCGAGCACCTTCGGTGAGATCAGCATTTCTTAACATTA 1681
QY 1787 TAGCAGCAGGAGGAGAAACCGTGAACCTGCAATGCGCAATGCGTGGCCACCGGTTGCAATC 1846
DB 1682 AAGGAGCAAGCTGGCAATGCAAGACGGCCAAATATTAAAGTATTGGCTACTCAGACC 1741
QY 1847 TTTTAACTCTAGACAAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTTATCCAGATTTCTGAAA 1906
DB 1742 TGTTCTGCTCTCAAAAGATGACCTCATGTGAAGCTCTAACTGAGTACCCAGATGCCAAA 1801
QY 1907 GGAATCTCATGAGAAAGCAGAGTGCTTTTAAACAGCAAGGCT 1950
DB 1802 CTATGCTAGAGAAAAAGGAAGCAAAATTTTAAATGAAAGATGGT 1845

RESULT 12

ADR24566
ID ADR24566 standard; DNA; 2500 BP.

XX
AC ADR24566;

XX
DT 21-OCT-2004 (first entry)

XX
DE Breast cancer prognosis marker #427.

XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.

XX
OS Homo sapiens.

XX
PN WO2004065545-A2.

XX
PD 05-AUG-2004.

XX
PF 15-JAN-2004; 2004WO-US001100.

XX
PR 15-JAN-2003; 2003US-00342887.

XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.

XX
PA (NECA-) NETHERLANDS CANCER INST.

XX
PI Van't Veer LJ, He Y;

XX
PI WPI; 2004-593473/57.

XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.

XX
PS Disclosure; SEQ ID NO 427; 226pp; English.

XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

XX
SQ Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;

Query Match 7.3%; Score 176.4; DB 13; Length 2500;

Best Local Similarity 49.6%; Pred. No. 1.5e-28;

Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;

QY 740 CAGACACATACACTACTGCGTTATTGGGACATCATATGTGATATCATCTACCTTTATG 799

DB 605 CTGATTACCTAGAAATTTGGTCAITTTGGATTAGGTATCAGATCATGATCTATTATTCG 664

QY 800 ATATGCTATTATTCAGCCCGCAGATCCAGTTTGTAAAGAGGAGAGACATAATAGTGGATT 859
DB 665 ATATG---TTTGTACGAACAAGGACAGCTTACCTAGAAACAAGGACTGCTGGTAAAGGAAG 721
QY 860 CAATGAGCTTAAGGAACACTACAGGACTTCTACAAAATTTTCAGTTGATGCTCGCATCAA 919
DB 722 AACTTAAACTCATAAATAAATATAAATCAAACCTTGCATTTTAAATCTGATGTTCTGTGTCAC 781
QY 920 TAATACCAATTTGATATTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTAGAGCAA 976
DB 782 TGATACCAACTGATTTGCTGTATTTAAAGTTAGGTTAGGTTGAACATATCCAGAAATAGATTAA 841
QY 977 ATAGATGTTAAAGTACACTTCATTTTGAATTTTAATCATCATCCTAGAGTCTATAATGG 1036
DB 842 ACAGGTTGTTACGGTTCTCTCGTATGTTGAGTTCTTCCAGAGAACAGAAACAAGGACAA 901
QY 1037 ACAAAGCATATATCTACAGAGTTATTGAAACAACCTGGATCTGCTGTTTATTCTGCACA 1096
DB 902 ACTATCCAAACATCTTCAAGATTTTCAACCTTGTATGTATATGTCATCATTTATCCACT 961
QY 1097 TTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1156
DB 962 GGAATGCTGTGTTCTACTCTATTTCTAAAGCTATTGGAATTTGGAATGATACATGG 1021
QY 1157 TGTG-----TGATGGGGAAGAAACGAGTATCTGAGATGTT 1192
DB 1022 TCTACCTGATATTAATGATCCTGAATTTGGCCGTTTGGCTAGAAAATACGTATACAGCC 1081
QY 1193 ATTATGGGAGTTGGAACCTTTAATTAACCTTGTGGCTTCCAGAACCAACAACCTTTAT 1252
DB 1082 TTTACTGGCTACACTGACTTTGACTACCATTTGTTGAAACACCCCTCCCTGAGGGGAT 1141
QY 1253 TTGAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTCTGTTCTTCCAGTTTAA 1312
DB 1142 CTGATATGCTTTGTTGGTGTGATTTCTTAATTTGGAGTGTAAATTTTCTACCATCG 1201
QY 1313 TTGTCAGATGAGAGATGTTGAGAGAGCTACAGCCAAATCAGAACTACTTTCGCGCT 1372
DB 1202 TTGTTAAACATAGGTTCTATGATTTTCAACATGAATGCAGCCAGAGCAAAATTTCAAGCAA 1261
QY 1373 GCATGGATGACACCATTTGCCCTACATGAACAATTAATCTCCATTCCTTAATCTGCGAAAGC 1432
DB 1262 GAATTGATGCTATCAAGCAATATATGCAATTTTCAAAATGTAAAGCAAGATATGGAAGA 1321
QY 1433 GAGTTCCGACTTTGTTATGAATATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATT 1492
DB 1322 GGGTTATTAATGTTTGAATCTCTGTTGGACCAACAACAAAACAGTTGATGAGAAAGAG 1381
QY 1493 TGCTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTCGCCATTTGATGTGAATTTTCAAG 1552
DB 1382 TCTTAAAGTATCTACCTGATAAACTAAGAGCAGAAATTTGCCATCAACGTTCACTTAGACA 1441
QY 1553 TCATCAGCAAGTCCGACTTTGTTCAAGGTTGTGATACACAGATGATTATACATGTTGC 1612
DB 1442 CATTAAGAAAGGATGAGCAATTTTCTGATTTGAAGCTGGTCTGTGGTGGATGTTGGTCT 1501
QY 1613 TAAGATTGAATCCGTTCTCTATTGCTGTGTGATTTGCTGCAAAAAGGAGAGAAATTTG 1672
DB 1502 TGAATTTGCAACCCCAAGTCTACAGTCTGAGGATATATTTTGAAGAAAGGGATATCG 1561
QY 1673 GCAAGGAAATGATATATCATCAAGCATGGAAGTCCCAAGTTCTTTGGAGGCCCTGATGTA 1732
DB 1562 GACGAGAGATGTCATATTATCAAGGAGGCAAACTCGCTGTGGTGGCAGATGATGGAGTCA 1621
QY 1733 CTAAAGTTCTGGT-----TACTCTGAAGAGTGGGTGGGTGGGAGAAATC--AGCCTTC 1786
DB 1622 CTCAGTTTGTGTTATGAGCGATGCGCAGCACTTTCGGTGAGATCAGCATTTCTTAACATTA 1681
QY 1787 TAGCAGCAGGAGGAGGAAACCGTGAACCTGCAATGTTGGTGGCCACCGGTTTTCGCAATC 1846
DB 1682 AAGGAGCAAGCTGGCAATGCAAGAACGGCCAAATATAAAGTATTGGCTACTCAGACC 1741
QY 1847 TTTTAACTCTAGACAAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTTATCCAGATTTCTGAAA 1906

Db 2 TGGTGGTCTCCTGTCACAACTTCTGGTGATTAATCTACCGCTTCGGCTTCC 61
Qy 728 CATATCAAAACGCGACACATACACTACTGGCTTTATTGCGGACATCATATGTGATATCA 787
Db 62 AGGAGATCAATCGGGGAACGATCGCAATTTGGTCTGTCTGACTTACCTGCGACTTCC 121
Qy 788 TCTACCTTTATGATATGATTTATTCAGCCAGACTCCAGTTTGTAGAGAGGAGACA 847
Db 122 TGTATCTGATCGATATACTGT---TCCACTTTCGCACCGGATACCTGGAGACCGGGTGC 178
Qy 848 TAATAGTGGATCAAAATGAGCTAAGGAACACTACAGGACTTCTACAAAATTTTCAGTTGG 907
Db 179 TGCAGACGAGCTTTGAAGCTGCGCACCCACTACATGAATCGACGATCTTCTACATCG 238
Qy 908 ATGTGCGCATCAATATACCAATTTGATATTTGCTACTCTCTCTTTGGGTTTAAATCCAATGT 967
Db 239 ACTGCTGTGCTGCTGCGGCTGGACTTTCTATTGCTCCATCGCTTTAACTCGATCC 298
Qy 968 TTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTGGAAATTTAATCATCACCTAGAGT 1027
Db 299 TGCAGAGCTTCCGGCTGGTGAAGATCTACCGGTTCTGGGCCCTTCATGATCGCACCGAGC 358
Qy 1028 CTATAATGGACAAAGCATATATACAGAGTTATTGGAACACTGGATCTGCTGTTTA 1087
Db 359 GGCACACCACTACCCGAACTGTTCCGGAGCAGCGCCCTCATCCACTACTCTGTTGTA 418
Qy 1088 TTCTGCATTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAAATTTGGCACTA 1147
Db 419 TATTCCATTGGAACGGTTGTCTTACCACATCATACACAAACAATGGGTTCCGATCAC 478
Qy 1148 CTAGATGGGT-----GTATGATGGGGAAGAAACGAGTATCTGAGATGTT 1192
Db 479 GCAACTGGGTCTACCCAGACTCGGAGTCGGGAGCTGGTCAAGCAGTATCTGCGAGCT 538
Qy 1193 ATTATGGGAGTTGCAATTTAATACCATTTGTTGGCTTCCAGAACCAAACTTTAT 1252
Db 539 ACTACTGGTGACCTTGGCCCTTGACCACTCGGGGATCTTCCCAAGCGCGCTCCAAGG 598
Qy 1253 TTGAAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTGTGTTCTCCAGTTTAA 1312
Db 599 GCGAGTACGTTTGTATCTCGAGCTGCTTTGGCTGATGCTTTCGCCACGGTAC 658
Qy 1313 TTGTTCAGATGAGAGATGATGAGAGCTACAGCAATCAGAACTACTTTCGGCGCT 1372
Db 659 TGGGCGACGTGGCCAACTTGTGAGTCACTGAGTGACGCGCAAGAGTTTCAAGCCA 718
Qy 1373 GCATGGATGACACCATGCTTACATGAACATTTACTCCTTAAACTTTGCGAAAGC 1432
Db 719 AGCTGGATGGCGTGAAGACGTACATGCGGATGCGACGTTGTCGGAATCATCTGCGGTGA 778
Qy 1433 GAGTTGCGACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATT 1492
Db 779 AGGTCAATCAATGGTTGATTAACCTGTGGCTTACGCAAAATGCTCGACAGGAGCGCG 838
Qy 1493 TGCTTAAGACCTTACCACTACGTTCCAGTTAGCCCTCGCCATGATGTAACCTTCAGCA 1552
Db 839 CCGTGTCTGCTCTCTGATAAATTAAGGCTGAATAGCAATTAACGTCATTTAGATA 898
Qy 1553 TCATCAGCAATGCTACTGTTTCAAGGTTTGTGATACACATGATTTATGACATGTTGC 1612
Db 899 CGCTCAAGCGGTTGGAGATTTTCCAAAACACAGAGGCGCGCTTCTATGCGAATCTGGTGC 958
Qy 1613 TAAGATTGAATTCGTTCTTCTATTGCTGCTGAGCTTTGTCGAAAAGGAGAAATTTG 1672
Db 959 TGGCGCTGAGCGCGTGTCTCTCTGCGCCGCGACTACATCTGCAAGAGGCGAGGTGG 1018
Qy 1673 GCAAGGAATGATATATCAATCAAGCATGGAGAGTCCAAAGTTCTTTGGAGGCCCTGATGTA 1732
Db 1019 GCAAGGAGATGTACATTTGTGAACGAGGACGATGTCAGTTGGTGGCGAGGTGG 1075
Qy 1733 CTAAGTTCTGGTTACTCTGAAAGCTGGGTGCGTGTGTTGGAGAAATCAGCCTTCTAGCAG 1792
Db 1076 AGACGGTATGGCCTCCCTGGAAGGTGTTCTCTATTTTTGGCGAGATTAGTATACTCAATA 1135

Qy 1793 CAGG---AGGAGAAACCGTGGAACTGCCAATGTGGTGGCCCAACGGGTTTCCCAATCTTT 1849
Db 1136 TGGGCACCGCAGGCAACCGACGACAGCCGCTTGCCTCAGTGGGATACAGCGACTCT 1195
Qy 1850 TAACTCTAGACAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTTATCCAGATTTCTGNAAGGA 1909
Db 1196 TCGTCCCTGAGCAAGAAGACATGTGGGACGTGCTGAAAGAGTATCCGCGCGCGGTGTTTC 1255
Qy 1910 TCCTCATGAAGAAAGCAGAGTGTCTTTTAAAGCAAGAGGCTTAAGACCCG 1958
Db 1256 GTCTGGAGTCGATAGCCGTCAGCGATTGGAGAAATACAGAAGGCCCC 1304

RESULT 15
ADFS6505
ID ADFS6505 standard; DNA; 3027 BP.

XX ADFS6505;
XX 12-FEB-2004 (first entry)
XX Modified rat olfactory cyclic nucleotide-gated ion channel DNA #1.
XX ds; gene; olfactory cyclic nucleotide-gated ion channel;
XX increased cAMP sensitivity; decreased cGMP sensitivity;
XX decreased nitric oxide sensitivity;
XX decreased calcium-calmodulin sensitivity.
XX Rattus norvegicus.

Key Location/Qualifiers
CDS 340..2334
/*tag= a

US2003157571-A1.
21-AUG-2003.
15-NOV-2002; 2002US-00295573.
16-NOV-2001; 2001US-0332494P.
(COLS) UNIV COLORADO.
Karpen JW, Rich TC, Cooper DMF, Schaack J;
WPI; 2003-787336/74.
P-PSDB; ADFS6501.
New nucleic acid encodes modified olfactory cyclic nucleotide-gated ion channels which exhibit increased sensitivity and specificity for cAMP and are useful to elucidate activities of proteins important in cAMP signaling.

Disclosure; SEQ ID NO 1; 63pp; English.
The invention relates to an isolated nucleic acid encoding a modified olfactory cyclic nucleotide-gated ion channel, where the channel comprises mutations which together impart increased cAMP sensitivity and decreased cGMP sensitivity, decreased nitric oxide sensitivity and decreased calcium-calmodulin sensitivity. The invention is used to elucidate activities of receptors, G-proteins, phosphodiesterases, adenylyl cyclases and other proteins important in cAMP signaling. The present sequence represents modified rat olfactory cyclic nucleotide-gated ion channel DNA.
SQ Sequence 3027 BP; 783 A; 698 C; 746 G; 800 T; 0 U; 0 Other;

Query Match 5.58; Score 133.2; DB 10; Length 3027;
Best Local Similarity 46.8%; Pred. No. 5e-19;
Matches 623; Conservative 0; Mismatches 673; Indels 36; Gaps 5;

1	2049.4	84.3	2135	4	US-09-949-016-1074	Sequence 1074, Ap
2	2035.4	83.8	2139	4	US-09-949-016-5798	Sequence 5798, Ap
3	330	13.6	99370	4	US-09-949-016-12816	Sequence 12816, A
4	330	13.6	99370	4	US-09-949-016-17540	Sequence 17540, A
5	329.6	13.6	601	4	US-09-949-016-38930	Sequence 38930, A
6	329.6	13.6	601	4	US-09-949-016-38931	Sequence 38931, A
7	329.6	13.6	601	4	US-09-949-016-205286	Sequence 205286, A
8	329.6	13.6	601	4	US-09-949-016-205287	Sequence 205287, A
9	202	8.3	601	4	US-09-949-016-38898	Sequence 38898, A
10	202	8.3	601	4	US-09-949-016-205176	Sequence 205176, A
11	181.2	7.5	2796	4	US-09-949-016-5678	Sequence 5678, Ap
12	169.8	7.0	84571	4	US-09-949-016-17420	Sequence 17420, A
13	151.4	6.2	601	4	US-09-949-016-38897	Sequence 38897, A
14	151.4	6.2	601	4	US-09-949-016-205175	Sequence 205175, A
15	147.6	6.1	601	4	US-09-949-016-38915	Sequence 38915, A
16	147.6	6.1	601	4	US-09-949-016-205232	Sequence 205232, A
17	144.6	6.0	601	4	US-09-949-016-205228	Sequence 205228, A
18	144.6	6.0	601	4	US-09-949-016-205229	Sequence 205229, A
19	143	5.9	601	4	US-09-949-016-38929	Sequence 38929, A
20	143	5.9	601	4	US-09-949-016-205285	Sequence 205285, A
21	132.8	5.5	3470	4	US-09-949-016-4344	Sequence 4344, Ap
22	132.8	5.5	32666	4	US-09-949-016-16086	Sequence 16086, A
23	102.6	4.2	601	4	US-09-949-016-38918	Sequence 38918, A
24	102.6	4.2	601	4	US-09-949-016-205235	Sequence 205235, A
25	93.8	3.9	7218	1	US-08-232-463-14	Sequence 14, Appl
26	91.4	3.8	601	4	US-09-949-016-38908	Sequence 38908, A
27	91.4	3.8	601	4	US-09-949-016-205201	Sequence 205201, A


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QY 1166 GGAAGGAAACGAGTATCTGAGATGTTATTATTGGCAGTTCGAACTTTAAATTACCATGG 1225
Db 81122 GTTTGGCTAGAAATACGTATACAGCCCTTTACTGGTCTACACTGACTTTGACTACCATGG 81181
QY 1226 GTGGCCCTCCAGAACCAAACTTTTATTGTAATTTGTTTCAACTCTTGAATTTTTTTT 1285
Db 81182 GTGAAACACCCCTCCCGTGAGGATTCAGATGATGCTTTGTGGTGTGATTCTCTAA 81241
QY 1286 CTGGAGTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGTGATTGGAGCAGCTA 1345
Db 81242 TTGGAGTGTAAATTTTTTGTCTACCATCGTTGGTAAACATAGGTTCTATGATTTCCAACATGA 81301
QY 1346 CAGCCATCAGAACTACTTCGCGCCCTGTCATGATGACACCATTTGCTTACATAACAAT 1405
Db 81302 ATGACGACGAGCAGAAATTTCAAGCAAGAAATGATGCTATCAAGCAATATATGCAATTTTC 81361
QY 1406 ACTCCATTCCTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGGGACT 1465
Db 81362 GAAATGTAAGCAAGATATGCAAAAGAGGGTTATTAATGGTTTGACTACCTGTGGACCA 81421
QY 1466 CTCAAGAAATGCTAGATGATGATTTGCTTAAAGCCCTACCAACTACGGTCCAGTTAG 1525
Db 81422 ACAAAAACACAGTTGATGAGAAAGAGTCTTAAAGTATCTACCTGATAAATAAGAGCAG 81481
QY 1526 CCCTCGCATTGATGTGAACCTTCAGCATCATCAGCAAGTCGACTTTGTTCAAGGGTTGTG 1585
Db 81482 AAATGCCATCAACGTTTCACCTTAGACACATTAAGAGGTACGCATTTTGTGCTGATTTG 81541
QY 1586 ATACACAGATGATTTATGACATGTTGCTAAGATTTGAAATCCGTTCTCTATTTCCTGGTG 1645
Db 81542 AAGCTGCTGTTGGTGGAGTTGCTTGAATTTGCAACCCCAAGTCTACAGTCCCTGGAG 81601
QY 1646 ACTTGTCTGCAAAAGGAGAAATTTGGCAAGAAATGATATATCATCAAGCATGGAGAAG 1705
Db 81602 ATTATATTTCAGAAAGGGGATATCGACGAGAGATGTACATTTATCAAGGAAGGCAAC 81661
QY 1706 TCCAAGTCTTGGAGGCCCTGATGTACTAAAGTTCTGTTGTTTCTGTTGAAAGCTGGG 1761
Db 81662 TCCTGTGGTGGCAGATGATGGAGTCACTCAGTTTGTGGTATTGAGGATGGCAGTACT 81721
QY 1762 TCGGTGTTTGGAGAAATC--AGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTGCCA 1819
Db 81722 TCGGTGAGATCAGCAATTTTAAATTAAGGGAGCAAGCTGCAATCGAAGAACGCCA 81781
QY 1820 ATGTGTGGCCCAAGGGTTTGGCAATCTTTTAACTCTAGACAAAAAGACCCCTCCAAGAA 1879
Db 81782 ATATTAAGATATTGGCTACTCAGACCTGTTCTCTCTCAAAAGATGACCTCATGGAAG 81841
QY 1880 TTCTAGTGCAATATCCAGATTTCTGAAAGGATCTCATGAAGAACCCAGATGCTTTTAA 1939
Db 81842 CTCTAACTGATACCCAGATGCCAAACTATGCTGGAAGAAAGGGAAGCAGATTTTAA 81901
QY 1940 AGCAGAAGGCT 1950
Db 81902 TGAAGATGCT 81912
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RESULT 13

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US-09-949-016-38897/c
; Sequence 38897, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38897
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-38897
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Query Match 6.2%; Score 151.4; DB 4; Length 601;
Best Local Similarity 99.3%; Pred. No. 5.8e-29;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 493 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 552
Db 291 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 232
QY 553 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTAAAGCGAATT 612
Db 231 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTAAAGCGAATT 172
QY 613 AAACCTTCCAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAACAGCATAGATTCATACACAGGT 139
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RESULT 14

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US-09-949-016-205175/c
; Sequence 205175, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205175
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Query Match 6.2%; Score 151.4; DB 4; Length 601;
Best Local Similarity 99.3%; Pred. No. 5.8e-29;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 493 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 552
Db 291 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 232
QY 553 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTAAAGCGAATT 612
Db 231 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTAAAGCGAATT 172
QY 613 AAACCTTCCAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAACAGCATAGATTCATACACAGGT 139
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RESULT 15

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US-09-949-016-388915/c
; Sequence 38915, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38915
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38915

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Best Local Similarity 97.4%; Pred. No. 5.5e-28;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1456 ACATGGGACTCTCAAAGAAATGCTAGATGAGTCTG 1489
Db 481 ACATGGGACTCTCAAAGAAATGCTAGGTAAGCATG 448

Search completed: March 27, 2005, 18:08:32
Job time : 426 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 16:03:49 ; Search time 1277 Seconds
(without alignments)
11339.997 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 297965951 residues
Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2430	100.0	2703	11	US-09-855-828-2
3	2430	100.0	2657	11	US-09-855-828-16
4	577.4	23.8	4382	17	US-10-189-507-3
5	577.4	23.8	4382	17	US-10-159-563-147
6	306	12.6	680	13	US-10-027-632-204539
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8	176.4	7.3	2500	17	US-10-172-118-427
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10	133.2	5.5	3027	16	US-10-295-573-1
11	132.8	5.5	2085	15	US-10-345-680-27
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					Sequence 2, Appli
					Sequence 16, Appli
					Sequence 147, App
					Sequence 204539,
					Sequence 427, App
					Sequence 1, Appli
					Sequence 27, Appli

12	132.8	5.5	3486	15	US-10-345-680-25	Sequence 25, Appli
13	131.6	5.4	1995	15	US-10-087-217-1	Sequence 1, Appli
14	131.6	5.4	1995	15	US-10-087-217-5	Sequence 5, Appli
15	131.6	5.4	3027	16	US-10-295-573-2	Sequence 2, Appli
16	131.6	5.4	3027	16	US-10-295-573-4	Sequence 4, Appli
17	129	5.3	526	9	US-09-864-761-12975	Sequence 12975, A
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19	128.4	5.3	1995	15	US-10-087-217-7	Sequence 7, Appli
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25	111.2	4.6	1995	17	US-10-189-507-1	Sequence 1, Appli
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27	111.2	4.6	2190	14	US-10-029-677-23	Sequence 23, Appli
28	111.2	4.6	12017	9	US-09-735-927-3	Sequence 3, Appli
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33	82.6	3.4	336	18	US-10-674-124A-14888	Sequence 14888, A
34	81	3.3	625	13	US-10-027-632-179350	Sequence 179350,
35	80	3.3	625	17	US-10-027-632-179350	Sequence 179350,
C	79.8	3.3	492	18	US-10-674-124A-21270	Sequence 21270, A
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C	79.6	3.3	496	9	US-09-864-761-2534	Sequence 2534, Ap
C	79.2	3.3	37265	13	US-10-087-192-49	Sequence 49, Appli
C	79.2	3.3	39443	17	US-10-085-117-313	Sequence 313, App
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C	79	3.3	462	9	US-09-864-761-3829	Sequence 3829, Ap
C	79	3.3	1728	9	US-09-927-267-3	Sequence 3, Appli
45	79	3.3	1728	17	US-10-189-507-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-855-828-3
; Sequence 3, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Cresch, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human CNG3B coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION: CNG3B
US-09-855-828-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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361	GCTCCTGTTATAATAGATATGCGATGCCAGTCCAGCTACACAACTGGTGAAGAAGATCGGT	420
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RESULT 2

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US-09-855-828-2
; Sequence 2, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete human CNG3B nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2492)
; OTHER INFORMATION: CNG3B

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Qy	841	GGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTT	900
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Db	963	CAGTTGGAGTGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAAT	1022
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Db	1203	GGCACTACTAGATGGGTGTATGATGGGAAGGAAACGAGTATCTGAGATGTTATTATGG	1262
Qy	1201	GCAAGTTCGAATTTAATATACCATTTGTTGGCTTCCAGAACCTTATTTGAAAT	1260
Db	1263	GCAAGTTCGAATTTAATATACCATTTGTTGGCTTCCAGAACCTTATTTGAAAT	1322
Qy	1261	GTTTTTCAACTCTTGAATTTTTTTTCTCGAGTTTTTTGTGTTCTCCAGTTTAAATGTCAG	1320
Db	1323	GTTTTTCAACTCTTGAATTTTTTTTCTCGAGTTTTTTGTGTTCTCCAGTTTAAATGTCAG	1382
Qy	1321	ATGAGAGATGTGATTTGGAGAGCTACAGCAATCAGAACTACTTCGCGCGCTGCATGGAT	1380
Db	1383	ATGAGAGATGTGATTTGGAGAGCTACAGCAATCAGAACTACTTCGCGCGCTGCATGGAT	1442
Qy	1381	GACACATTCCTACATGACAAATTAATCTCCATTCCTTAAACTTGTGCAAAAGCGAGTTCG	1440
Db	1443	GACACATTCCTACATGACAAATTAATCTCCATTCCTTAAACTTGTGCAAAAGCGAGTTCG	1502
Qy	1441	ACTTGGTATGAAATATACATGGGACTCTCAAAGAAATGCTAGATGAGTCTGANTTGCCTAAG	1500

[illegible]

```

; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete CNG3B sequence derived from assembly of
; OTHER INFORMATION: PCR fragments
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(2541)
; OTHER INFORMATION: CNG3B
; US-09-855-828-16

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Query Match	100.0%;	Score 2430;	DB 11;	Length 2757;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2430;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTTTAAATCGCTGACAAAAGTCAACAAGTGAAGGCTATAGSAGAGAGACAATGAGAAT	60	
DB	112	ATGTTTAAATCGCTGACAAAAGTCAACAAGTGAAGGCTATAGSAGAGAGACAATGAGAAT	171	
QY	61	GAACAAAAGTTCTCGTCGGAATGAAGAAGGCTCTCACCCAAAGTAACTAGTCTCAGCAAAACC	120	
DB	172	GAACAAAAGTTCTCGTCGGAATGAAGAAGGCTCTCACCCAAAGTAACTAGTCTCAGCAAAACC	231	
QY	121	ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAACCAAGTCAATCTCAGTC	180	
DB	232	ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAACCAAGTCAATCTCAGTC	291	
QY	181	ACGTCTGAAGAGCCACACACACATACAGACAAACTCTCCAAAGAAAATTCCTCTTGGA	240	
DB	292	ACGTCTGAAGAGCCACACACACATACAGACAAACTCTCCAAAGAAAATTCCTCTTGGA	351	
QY	241	GATCTGACCAAAACCCCTGACCCCTCAAATATGCAGCAGAACCAACTGGAAACAGTCCCAAG	300	
DB	352	GATCTGACCAAAACCCCTGACCCCTCAAATATGCAGCAGAACCAACTGGAAACAGTCCCAAG	411	
QY	301	CAGAAGGAAATGGACCCCGGAAAGAGGTCCAAACAGCCACAAAAACAACCCGCTGCA	360	
DB	412	CAGAAGGAAATGGACCCCGGAAAGAGGTCCAAACAGCCACAAAAACAACCCGCTGCA	471	
QY	361	GCTCTGTTTAAATGATGATGCGGATGCCAGTCCCGAGTACACACCTGGTGAAGAGATCGGT	420	
DB	472	GCTCTGTTTAAATGATGATGCGGATGCCAGTCCCGAGTACACACCTGGTGAAGAGATCGGT	531	
QY	421	CAAGAGAACAGCCCTCTACAGAAAAGTGTGGTAGAGGAGATCTCTCTCACCCGAAAGCC	480	
DB	532	CAAGAGAACAGCCCTCTACAGAAAAGTGTGGTAGAGGAGATCTCTCTCACCCGAAAGCC	591	
QY	481	AGCCCCAACAATGCAAAAGCCCAAGGCTGTACCAAGTAAAGAAAGCGATGTAAGCCA	540	
DB	592	AGCCCCAACAATGCAAAAGCCCAAGGCTGTACCAAGTAAAGAAAGCGATGTAAGCCA	651	
QY	541	ACAGAACATTTACTACAGCGTGTGTTGGTTCAAAGTCAAAAAGATGCCCTTTAACAGAGTAC	600	
DB	652	ACAGAACATTTACTACAGCGTGTGTTGGTTCAAAGTCAAAAAGATGCCCTTTAACAGAGTAC	711	
QY	601	TTAAAGCGAATTTAAACTTTCCAAACAGCATAGATTTATACACAGATCGACTCTATCTCTCTG	660	
DB	712	TTAAAGCGAATTTAAACTTTCCAAACAGCATAGATTTATACACAGATCGACTCTATCTCTCTG	771	
QY	661	TGGCTCTTGCTGTGTCACCTCTTGCCCTAACTGGAACTGCTGGTTTATACCACTGGCGCTC	720	

Db 1322 GGGTATTAAATGGTTGACTACCTGGACCAACAAAAACAGTGTATGAGAAG 1381
 Qy 1493 TGCCTTAAGACCTTACCACTACGGTCCAGTTAGCCCTGCCATTCATGTGAATTCAGCA 1552
 Db 1382 TCTTAAAGTATCTACCTGATAACTAAGGACGAAATGGCCATCAAGCTTCACTTAGACA 1441
 Qy 1553 TCATCAGCAAGTCGACTGTGTTCAAGGGTGTGATACAGAGATGATTTATGACATGTTGC 1612
 Db 1442 CATTAAAAAGGTACGCATTTTGTGCTGATTTGTAAGCTGGTCTGTTGGTGGATGGTCT 1501
 Qy 1613 TAAGATTGAATCCGTTCTTATTTTGGCTGGTGAATTTGTCGCAAAAGGGAGAAATG 1672
 Db 1502 TGAATTTGAACCCCAAGTCTACAGTCTGGAGATATATTTGCAAGAAAGGGGATATCG 1561
 Qy 1673 GCAAGGAATGTATATCAATCAAGCATGGAGAGTCCAAGTCTTGGAGCCCTGATGGTA 1732
 Db 1562 GACGAGAGATGTACATTTCAAGGAGGCAAACTCGTGTGGTGCAGATGATGAGTCA 1621
 Qy 1733 CTAAAGTCTGTGTTTACTCTGAAGCTGGGTGGTGGTGGAGAAATC--AGCCTTC 1786
 Db 1622 CTCAGTTGTGTTATGAGCGATGGCAGCACTTCGGGTGAGATCAGCATTTCTTAACATTA 1681
 Qy 1787 TAGCAGCAGGAGGAGAAACGTCGAATGCCAATGTGGTGGCCACCGGTTGGCAATC 1846
 Db 1682 AAGGAGCAAAAGCTGGCAATCGAAGACGGCCAAATTTAAAGTATTTGGCTACTCAGACC 1741
 Qy 1847 TTTTAACTCTAGACAAAAAGACCTCCCAAGAAATCTAGTCATTTCCAGATTCAGAAA 1906
 Db 1742 TGTCTGTCTCTCAAAAGATGACCTCATGGAAGCTCTAAGTGTACCAAGATGCCAAA 1801
 Qy 1907 GGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGCT 1950
 Db 1802 CTATGCTAGAAGAAAAAGGAAGCAAAATTTTAAATGAAAGATGGT 1845

RESULT 9

US-10-342-887-427
 ; Sequence 427, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; PRIORITY FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 427
 ; LENGTH: 2500
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-342-887-427

Query Match 7.3%; Score 176.4; DB 17; Length 2500;
 Best Local Similarity 49.6%; Pred. No. 1.1e-27;
 Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;
 Qy 740 CAGACACATACACTACTGCTTATTCGGGACATCATATGTGATATCATCTACCTTTATG 799
 Db 605 CTGATTACCTAGAATATTGGTCTATTTGGATTACGTATCAGACATAGTCTATTAAATCG 664

Qy 800 ATATGCTATTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGACATAATAGTGGATT 859
 Db 665 ATATG---TTGTAGCAACAAGGACAGGTACCTAGAACAAAGGACTGCTGGTAAAGGAAG 721
 Qy 860 CAATGAGCTAAGGAAACACATACAGGACTTCTACAAAATTTTCAGTTGATGTCGATCAA 919
 Db 722 AACTTAAACTCATAAATAAATATAAATCCAACTTTGCAATTTTAAACTTGTATGTTCTGTCC 781
 Qy 920 TAAATACCATTTGATATTTGCTACCTCTTCTTTTGGGTTTA---ATCCAATTTTGTAGACAA 976
 Db 782 TGATACCAACTGATTTGCTGTATTTTAAAGTTAGGGTGGAACTATCCAGAAATATGATTTAA 841
 Qy 977 ATAGAGTGTAAAAGTACACTTTCATTTTGTGAATTTAATCATCACCTAGAGTCTATAATGG 1036
 Db 842 ACAGTTGTTACGGTTCCTCTCGTATGTTTGTAGTTCTCCAGAGAACAAGGACAA 901
 Qy 1037 ACAAAGCATATATCTACAGAGTTATTCGAACAACCTGGTACTTGTGTTTATTTCTGACACA 1096
 Db 902 ACTATCCAAACATCTTTCAGGATTTTCCAACTTTGTTATGTATATCGTCACTATTCCTACT 961
 Qy 1097 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATGG 1156
 Db 962 GGAATGCAATGTGTTTCTACTCTATTTCTAAAGCTATTTGGAAATGATACATGG 1021
 Qy 1157 TGTA-----TGATGGGGAAGGAAACGAGTATCTGAGATGTT 1192
 Db 1022 TCTACCTGATATTAATGATCCTGAATTTTGGCCGTTTGGCTAGAAAAATACGTATACAGCC 1081
 Qy 1193 ATTAATGGGAGTTTCGAACCTTTAATACCTATGGTGGCTTCCAGAACCAAACTTTAT 1252
 Db 1082 TTTACTGCTCTACACTGACTTTTGACTACCAATTTGGTGAACACCCCTCCCGTAGGGATT 1141
 Qy 1253 TTGAAATTTGTTTTCAACTCTTGAATTTTCTGGAGTTTCTGTTCTCCAGTTTAA 1312
 Db 1142 CTGATATGTTTGTGGTGGTGTGATTTCTTAATTTGGAGTGTAAATTTTGTCTCATCG 1201
 Qy 1313 TTGTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCAAATCAGAACTACTTCCCGGCT 1372
 Db 1202 TTGGTAACATAGTTCTATGATTTTCCAACATGAATGCAGCCAGAGCAAGATTTCAAGCAA 1261
 Qy 1373 GCATGGATGACACCATTTGCTTACATGAACAATTTACTCCATTTCTTAACTTTGTGCAAAAGC 1432
 Db 1262 GAATTTGATGCTATCAAGCAATATATGCAATTTTCGAAATGTAAAGCAAGATATGAAAAAGA 1321
 Qy 1433 GAGTTCCGACTTGTGATGAATATACATGGGACTCTCAAAGAAATGCTAGATGATCTGATT 1492
 Db 1322 GGGTTATTAATGTTTGTACTCTCTGAGACCAACAAAAAACAGTTTGTAGAAAAAG 1381
 Qy 1493 TGCTTAAAGACCTTACCAACTACGGTCCAGTTTAGCCCTCGCCATTCATGTAACCTTCAGCA 1552
 Db 1382 TCTTAAAGTATCTACTGTATTAACCTAAGAGCAGAAATTTGCCATCAACGTTCACTTAGACA 1441
 Qy 1553 TCATCAGCAAGTGCATTTGTTCAAGGGTGTGATACAGATGATTTATGACATGTTTGC 1612
 Db 1442 CATTAAAAAGGTACGCATTTTCTGCTGATTTGTAAGCTGGTCTGTTGGTGGATGGTCT 1501
 Qy 1613 TAAGATTGAATCCGTTCTTATTTTGGCTGGTGAATTTGTCGCAAAAGGGAGAAATG 1672
 Db 1502 TGAATTTGCAACCCCAAGTCTACAGTCTGAGATATATTTTGAAGAAAGGGGATATCG 1561
 Qy 1673 GCAAGGAATGTATATCATCAAGCATGGAGAAATTTTAAAGTCTTGGAGCCCTGATGGTA 1732
 Db 1562 GACGAGAGATGTACATTTCAAGGAGGCAAACTCGTGTGGTGGCAGATGATGAGTCA 1621
 Qy 1733 CTAAAGTCTGTGTTTACTCTGAAGCTGGGTGGTGGTGGAGAAATC--AGCCTTC 1786
 Db 1622 CTCAGTTGTGTTATGAGCGATGGCAGCACTTCGGGTGAGATCAGCATTTCTTAACATTA 1681
 Qy 1787 TAGCAGCAGGAGGAGAAACGTCGAATGCCAATGTGGTGGCCACCGGTTTGGCAATC 1846
 Db 1682 AAGGAGCAAAAGCTGGCAATCGAAGACGGCCAAATTTTAAAGTATTTGGCTACTCAGACC 1741

Qy	1847	TTTTAACTCTAGACAAAAGACCTCCAAGAAATCTTAGTGCATATATCCAGATTCGAAA	1906
Db	1742	TGTTCTGTCTCTCAAAAAGATGACCTCATGGAAGCTCTAACTGAGTACCCAGATGCCAAA	1801
Qy	1907	GGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGGCT	1950
Db	1802	CTATGCTAGAAAGAAAAGGGAAGCAAAATTTTAAATGAAAGATGGT	1845

RESULT 10

US-10-295-573-1

: Sequence 1. Application US/10295573

: Publication No. US20030157571A1

GENERAL INFORMATION:

; APPLICANT: Karpen, Jeffrey W.

APPLICANT: Rich, Thomas C.

; APPLICANT: Cooper, Dermot M.F.

APPLICANT: Schaack, Jerome

10 TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS

FILE REFERENCE: UTC-07536

; CURRENT APPLICATION NUMBER: US/10/295,573

; CURRENT FILING DATE: 2002-11-

; PRIOR APPLICATION NUMBER: 60/332,494

;
PRIOR FILING DATE: 2001-
ATTORNEY OF RECORD: 2001-01-01

; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: Patent in version 3.1
; CFC ID NO. 1

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; SEQ ID NO 1

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; LENGTH: 3027
; TYPE: DNA

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TYPE: DNA
ORGANISM:

ORGANISM: RALLUS NORVEGICUS;
IIS-10-295-573-1

T-3/E-667-01-80

Query Match 5.5%: score 133.2: DB 16: length 3027:

Query Match	5.58;	Score	133.2;	Length	3027;
Best Local Similarity	46.8%;	Pred. NO.	2.7e-18;		
Matches	623;	Conservative	0;	Mismatches	673;
				Indels	36;
				Gaps	5;

652	QY	TATCTCTGTGGCTCTTGCTTGTCAC	711	TATCTCTGTGGCTCTTGCTTGTCAC
763	Db	TATTTACCGTTGGTTGTTGTCAT	822	TATTTACCGTTGGTTGTTGTCAT
712	QY	CTGGCCCTGCTTCCCATATCAAA	771	CTGGCCCTGCTTCCCATATCAAA
823	Db	GCACAGCCTGCTTCAGTGATCT	882	GCACAGCCTGCTTCAGTGATCT
772	QY	ATCATATGTGATATCATCTTACT	831	ATCATATGTGATATCATCTTACT
883	Db	TACTTCTCAGACACTGTCATAT	939	TACTTCTCAGACACTGTCATAT
832	QY	GTAAGAGGAGGAGACATAAAT	891	GTAAGAGGAGGAGACATAAAT
940	Db	CTAGAACAGGGGCTCTTGGTCA	999	CTAGAACAGGGGCTCTTGGTCA
892	QY	ACAAAATTCAGTTGGATGTCG	951	ACAAAATTCAGTTGGATGTCG
1000	Db	TTGCAGTTCAAAATGGAGTG	1059	TTGCAGTTCAAAATGGAGTG
952	QY	GGGTT---TAATCCAATGTTT	1008	GGGTT---TAATCCAATGTTT
1060	Db	GGTATCCACAGCCTGAGGTAC	1119	GGTATCCACAGCCTGAGGTAC
1009	QY	TTTAAATCATCACCTAGAGTCT	1068	TTTAAATCATCACCTAGAGTCT
1120	Db	TTCTTTGACCGCACTGAGAC	1179	TTCTTTGACCGCACTGAGAC
1069	QY	ACTGGATACATTCGCTGTTTAT	1128	ACTGGATACATTCGCTGTTTAT
1180	Db	GTCCCTTTACATCTTGGTCAT	1239	GTCCCTTTACATCTTGGTCAT
1129	QY	TATGAAGGAATTGG-----	1164	TATGAAGGAATTGG-----
1240	Db	TCCATTTGGCTTTGGAGTTG	1299	TCCATTTGGCTTTGGAGTTG
1165	QY	GGGGAAGGAAACGAGTATCT	1224	GGGGAAGGAAACGAGTATCT

1429 AAGCGAGTTCGGACCTTGGTATGAAATATATACATCCGACCTCTCAACGAAATCGCTACATCACTCT 1488

Query Match 5.5%; Score 132.8; DB 15; Length 3486;
Best Local Similarity 49.2%; Pred. No. 3.6e-18;

?	OTHER INFORMATION:				
	US-10-087-217-5				
	Query Match	5.4%;	Score 131.6;	DB 15;	Length 1995;
	Best Local Similarity	46.7%;	Prod.No. 5e-18;		
	Matches 622;	Conservative 0;	Mismatches 674;	Indels 36;	Gaps 5;
Qy	652	TATCTCCTGTGGCTCTTGTCTGTGTCACCTCTTGGCCTATAA	CTTAACTGGAAC	TGCTGCTTTATACCA	711
Db	424	TATTACCGTTGGTGTGTTGTGTCATTGGCATGCCTGTTCTTT	TACAAC	TGGTGCCTGTTGGTG	483
Qy	712	CTGGGCGCTGCTTCCCATATCAAAACGGCAGACAACATACAC	TACTACTGCTTATTCGGGCTTATTCGGGAC	771	
Db	484	GCCAGAGCCTGCTTTCAGTGATCTACAGAGAAACTATTTTG	TGGTATGGCTGGTCTGGAC	543	
Qy	772	ATCATATGTGATATCATCTACCTTTTATGATATGCTATTTAT	CCAGCCAGAC	TCCAGCTT	831
Db	544	TACTTCTCAGACACTGTCTATATCGCAGACCTCATCATTC	GGTGGCAGAGG	---	600
Qy	832	GTAAAGGAGGAGACATAATAGTGGATTCAAAATGAGCTAAG	AGAAAC	TACAGGACTTCT	891
Db	601	CTAGAACAGGGCTCTTGGTCAAAAGATCCCAAGAAATTCG	CAGACAACTATATTCACACT	660	
Qy	892	ACAAAATTTTCAGTTGATGTCGATCAATAATACCAATTTG	ATATTTGCTACTCTTCTTT	951	
Db	661	TTGCAGTTCAAAATGGATGTGGTCTTATCATTTCCCACTG	CACCTATCTATTTTGTCTGTG	720	
Qy	952	GGGTT---TAATCCAATGTTTAGAGCAATAGGATGTTAAAG	TACACTTCATTTTGTAA	1008	
Db	721	GGTATCCACAGCCTGAGGTACGCTTCAACCGCTATTTAC	ACTTTGCCCCGTATGTGTAG	780	
Qy	1009	TTTAAATCATCACCTAGAGTCTATAATGGACAAAGCATAT	CTACAGAGTTATTCGAACA	1068	
Db	781	TTCTTTGACCGCACTGAGACACGACCGACTACCCCAACAT	CTTCCGAATCAGCAATCTG	840	
Qy	1069	ACTGGAATCTGCTGTTTATTTGCAACATTAATGCTGTTT	TATTTACTGGGCTTCAAAC	1128	
Db	841	GTCTTTTACATCTTGCTGCATCATCCACTGGAATGCTGT	TATTTATTTATTTTCTTAAG	900	
Qy	1129	TATGAAGGAATGG-----	-----CACTACTAGATGGGTGTATGAT	1164	
Db	901	TCCATTTGGCTTTGGAGTTGACACTCGGGTTTACCCCAAC	ATTAAGCTGACCTGAATATGGC	960	
Qy	1165	GGGGAAGGAAACAGATATCTGAGATGTTATTTGGGCAGT	TTCGAAC	CTTTAAATACCATT	1224
Db	961	TACCTGGCTAGAGGTACATTTACTGCTTTACTGGTCCAC	ACTTGACCTCACCACCAT	1020	
Qy	1225	GGTGGCCTTCCAGAACCAAACTTTATTTGAAATGTTTTT	TCAACTCTTTGAAATTTTT	1284	
Db	1021	GGAGAGACACACCCCTGTAAAGGATGAGGAGTACCTAT	TTTGTCTCTTTGACTTCTTG	1080	
Qy	1285	TCGTGGAGTTTTGTGTTCTCCAGTTTAAITGGTCAGATG	AGAGATGTGATTTGAGCAGCT	1344	
Db	1081	ATTGGTGTCTCATCTTTGCCACTATTTGGGAAATGTGG	GCCTCCATGATCTCCAAACATG	1140	
Qy	1345	ACAGCCAATCAGAACTACTTTCCGCGCTGCATCGGATG	ACACCACTTGCTACATGAACAAT	1404	
Db	1141	AATGCCACAGGACAGATTCAGGCCAAGATTGATGCTGT	CAAACTACATGCAGTTC	1200	
Qy	1405	TACTCCATTTCTAACTTTGTGCAAAAACGAGTTTGGAT	GTGGTATGAATATACATGGGAC	1464	
Db	1201	CGAAAGGTGAGCAAGACATGGAAGCCAAGTTCATCAAT	TGGTTTGACTACTTTGTGGACC	1260	
Qy	1465	TCTCAAAGATGCTAGATGATCTGATTTGTCTTAAGAC	CCCTACCACACTACGTTCCAGTTA	1524	
Db	1261	AATAAGAAGACAGTAGATGAAACGAGAAGTCTCAAGAA	CCCTGCGCAGCAAGCTCAGGGCT	1320	
Qy	1525	GCCTCTGCCATTGATGTGAACTTTCAGCATCATCAGCA	AAAGTCGACTTTGTTCAAGGGTGTG	1584	
Db	1321	GAGATAGCCATTAAUGTTTCACTTGTCCACTCTGAA	GAAGTGGCGATATTTCCAGGATTTG	1380	
Qy	1585	GATACACAGATGATTTTATGACATGTTTGCTAAGAT	TGAAATTCGCTTCTATTTTGCCTGGT	1644	

Db 1381 GAAGCTGGCTACTGGTGGAACTGGTACTGAAGCTTCTGCTCAGGCTTTAGTCTCTGGA 1440
QY 1645 GACTTTGCTGCAAAAAGGAGAGAAATGGCAAGAAATGTATATCATCAAGCATGGAGAA 1704
Db 1441 GATTATATTTCCGTAAAGGGGACATTTGGCAAGAAATGTATATCATCAAGAGGGCAAG 1500
QY 1705 GTCCAAGTTCTTGGAGCCCTGATGTGTAATAAGTTCTGGT-----TACTCTGAAAGCTGG 1760
Db 1501 TTGGCAGTGGTAGCTGATGATGGTGACTCAGTATGSCCTTGCTCTCAGCTGGAGCTGC 1560
QY 1761 GTCGGTGTGGAGAAATACGCTTCTAGCAGCAGAGGA--GGAAACGTCGAACCTGCC 1818
Db 1561 TTTGGTGAGATTAGTATCTTAACTTAAGGGTAGCAAAATGGGCAATCGACGTACTGCT 1620
QY 1819 AATGTGTGGCCCAAGGTTTGGCAATCTTTAACTCTAGACAAAAGACCTCCAAGAA 1878
Db 1621 AATATCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAAGACGATCTTATGGAA 1680
QY 1879 ATTCTAGTGCATTAATCCAGATCTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTTTA 1938
Db 1681 GCTGTAACGTAGTATCTGATGCCAAGAGGTCTCTGGAGGAAGCGGGTAGGGAGATCCTTG 1740
QY 1939 AAGCAGAGGCT 1950
Db 1741 ATGAAGATGGGT 1752

RESULT 15
US-10-295-573-2
; Sequence 2, Application US/10295573
; Publication No. US2003015751A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schaack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS
; FILE REFERENCE: UTC-07536
; CURRENT APPLICATION NUMBER: US/10/295,573
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-295-573-2

Query Match 5.4%; Score 131.6; DB 16; Length 3027;
Best Local Similarity 46.7%; Pred. No. 6.1e-18;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;

QY 652 TATCTCTGTGGCTCTTGTCTTGTCACTCTTGSCCTATAAAGTGAACCTGCTGTTTATACCA 711
Db 763 TATTACGCTGGTGTGTTGTCATTGCCATGCTGTTCTTTACAACTGGTGCCTGTTGGTG 822
QY 712 CTGGCCTGCTCTCCCATATCAAAACCGGAGACAAATACACTACTGCTGCTTATGGCGAC 771
Db 823 GCCAGAGCCTGCTTCAAGTGTATACAGAGAACTATTTTGTGATGGCTGGTGGAC 882
QY 772 ATCATATGATATCATCTACCTTTTATGATGCTATTTATCATCGCCAGACTCCAGTTT 831
Db 883 TACTTCTCAGACACTGTGCTATATCGCGAGCCTCATANTTCGGCTGGCGACAGGC---TTC 939
QY 832 GTAAGAGGAGGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTTCT 891
Db 940 CTAGAACAGGGCTCTTTGTCAAAGATCCCAAGAAATGGGAGACAACTATATTCACACT 999
QY 892 ACAAATTTTCAGTTGGATGCGATCAATATACCAATTTGATATTTGCTACCTCTCTTT 951
Db 1000 TTGCAGTTCAAAATGGATGGGCTTCTATCATTTCCCACTGACCTTATCTATTTTGTGTG 1059

QY 952 GGGTT---TAATCCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAITTTTTTGA 1008
Db 1060 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTTCCCGTATGTTTGA 1119
QY 1009 TTTAATCATCACTAGAGTCTATATAGGAAAGCATATATCTACAGAGTTATTCAACA 1068
Db 1120 TTTCTTTGACCGCATGAGACACGACACCACTACCCCAACATCTTCCGAATACGAACTGT 1179
QY 1069 ACTGGATACCTGCTGTTTATTTCTGCACATTAATGCTGTGTTTATTACTGGGCTTCAAC 1128
Db 1180 GTCTTTTACATCTTGGTCAATCATCTCACTGGAATGCTTGTATTATTATGTTATTCTAAG 1239
QY 1129 TATGAAGGAATTTGG-----CACTACTAGATGGGTGTATGAT 1164
Db 1240 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCCAACATTAATGACCTGAATATGCC 1299
QY 1165 GGGGAAGAAACGAGTATCTGAGATGTTATTTATGGGCAAGTTCGAACCTTTAATATCAAT 1224
Db 1300 TACCTGGCTAGAGAGTACATTTTACTGCTCTTACTGCTCCACACTGACCTCACCACTT 1359
QY 1225 GGTGGCCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCACACTCTTGAATTTTTT 1284
Db 1360 GGAGAGACACCAACCTCTGTAAAGATGAGGAGTACCTATTGTTGTAATCTTTGACTTTG 1419
QY 1285 TCTGGAGTTTGTGTTCTCCAGTTTAAATTGGTTCAGATGAGAGATGTGATTTGGAGCAGCT 1344
Db 1420 ATTGGTGCTCTCATCTTTGCCACTATTGTTGGGAAATGTTGGGCTCCATGATCTCCAACATG 1479
QY 1345 ACAGCCAAATCAGAACTACTTTCGGCGCTGCATGGATGACACCAATTCCTTACATGAACAAT 1404
Db 1480 AATGCCACACGAGCAGAGTTCCAGGCCAAGATTGATGCTGTCAAAACACTACATACGATTC 1539
QY 1405 TACTCCATTCTAAACTGTCGAAAAGCGAGTTTCGACTTTGGTATGAATATACATCGGAC 1464
Db 1540 CGAAAGGTGAGCAAGACATGGAAGCAAGGTCATCAATGTTTGGCTTACCTTTGAGACC 1599
QY 1465 TCTCAAGAAATGCTAGATGAGTCTGATTTTGGCTTAAGACCTTACCACACTACGGTCCAGTTA 1524
Db 1600 AATAAGACACAGTAGATGAACGAGAGTCTCTCAAGAACCTGCCAGCAAGCTCAGGGCT 1659
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QY 1585 GATACACACATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTGTCCTGGT 1644
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QY 1761 GTCGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCTGCAACTGCC 1818
Db 1900 TTTGGTGAGATTAGTATCTCTTAACATTAAGGGTAGCAAAATGGGCAATCGACTACTGCT 1959
QY 1819 AATGTGGTGGCCCAAGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCTTCCAAGAA 1878
Db 1960 AATATCCGTAGCTGGGCTACTCAGATCTTCTGCTTGTCTCAAGGACGATCTTATGGAA 2019
QY 1879 ATTCTAGTGCATTAATCAAGTCTGAAAGATCTCTCATGAAGAAAGCAGAGTGTCTTTA 1938
Db 2020 GCTGTAACTGAGTATCTGATGCCAAGAGGTCTCTGGAGGAAAGCGGGTAGGGAGATCCTG 2079
QY 1939 AAGCAGAGGCT 1950
Db 2080 ATGAAGATGGGT 2091

Search completed: March 27, 2005, 20:53:32
Job time : 1286 secs

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 10:55:09 ; Search time 7048 Seconds
(without alignments)
13123.748 Million cell updates/sec

Title: US-09-855-828-3

Perfect score: 2430

Sequence: 1 atgtttaatcgtgacaaa.....aagaagaaggtaagaacataa 2430

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsi1:*

9: gb_gsi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	815.8	33.6	2056	3 AK040140	AK040140 Mus muscu
2	553	22.8	553	2 BF725470	BF725470 bx16c03.y
3	478	19.7	527	1 AL713036	AL713036 DKEP686A
4	477.4	19.6	1947	3 CR626336	CR626336 full1-1eng
5	470	19.3	655	2 BB635459	BB635459
6	430.2	17.7	437	2 BF725469	BF725469 bx16c03.x
7	402.4	16.6	881	2 BE287002	BE287002 601097229
8	363.8	15.0	1054	5 BX401127	BX401127 BX401127
9	320.8	13.2	468	1 AA069559	AA069559 zf75a04.r
10	320.8	13.2	656	5 BP224184	BP224184 BP224184
11	308.4	12.7	978	5 BQ068992	BQ068992 AGENCOURT
12	304	12.5	633	7 CR619966	CR619966 mk30e03.y
13	301.4	12.4	694	1 AU137778	AU137778 AU137778
14	286.8	11.8	741	5 BX104558	BX104558 BX104558
15	280.8	11.6	738	4 BI736222	BI736222 603359912
16	280	11.5	423	5 BM938767	BM938767 UI-N-CGOp
17	279	11.5	445	7 H53423	H53423 Yf86a09.r1
18	277.6	11.4	747	7 CR376265	CR376265
19	271.2	11.2	545	2 AW465556	AW465556 BP230019A
20	262.2	10.8	563	4 BG304577	BG304577 fl88b05.y
21	261.6	10.8	503	1 A1150392	A1150392 qf40g11.x
22	234	9.6	247	1 AA317961	AA317961 EST20020
23	232.4	9.6	270	1 AA012972	AA012972 ze35b03.r
24	224	9.2	325	2 BE982488	BE982488 UI-N-CGOp

25	219.6	9.0	823	7 CO814239	CO814239 AGENCOURT
26	219	9.0	696	5 BW269181	BW269181 BW269181
c 27	216.2	8.9	518	1 AV605886	AV605886 AV605886
28	216.2	8.9	747	4 BI733974	BI733974 603355503
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30	211	8.7	869	6 CD327412	CD327412 AGENCOURT
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32	197.2	8.1	581	1 AV605887	AV605887 AV605887
33	165.6	6.8	353	1 AL120448	AL120448 DKEP7611
34	164	6.7	376	1 AL120239	AL120239 DKEP761H
35	163.4	6.7	725	7 CR371016	CR371016 CR371016
c 36	162.2	6.7	674	9 CC498739	CC498739 CH240.335
37	137	5.6	832	4 BI827605	BI827605 603073571
c 38	131.2	5.4	591	9 CC571022	CC571022 CH240.446
39	129.8	5.3	573	4 BM354832	BM354832 rr17e02.y
c 40	120.6	5.0	535	1 AL928461	AL928461 AL928461
41	111	4.6	920	5 BU139545	BU139545 603133625
42	110.6	4.6	490	5 BQ633921	BQ633921 he21h09.y
c 43	109.2	4.5	584	5 BM882371	BM882371 ra99h10.y
44	108.8	4.5	777	7 CK477930	CK477930 AGENCOURT
45	106.8	4.4	819	5 BU287884	BU287884 603603670

ALIGNMENTS

RESULT 1	AK040140	AK040140	2056 bp	linear	HTC 03-APR-2004
LOCUS	AK040140	Mus musculus	0 day neonate thymus cDNA	RIKEN full-length enriched library, clone:A430069G05	product:cyclic nucleotide gated channel beta 3, full insert sequence.
DEFINITION	AK040140	HTC; CAP trapper..			
ACCESSION	AK040140.1	GI:26087649			
VERSION	AK040140.1	GI:26087649			
KEYWORDS	HTC; CAP trapper..				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	1 Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Method. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
AUTHORS	Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
TITLE	Genome Res. 10 (10), 1617-1630 (2000)				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi.N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaehiagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wachiagi,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
TITLE	Genome Res. 10 (11), 1757-1771 (2000)				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
AUTHORS	Functional annotation of a full-length mouse cDNA collection				
TITLE	Nature 409, 685-690 (2001)				
JOURNAL	Functional annotation of a full-length mouse cDNA collection				
MEDLINE	11076861				
PUBMED	11076861				
REFERENCE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research				

Group Phase I & II Team.	
Analysis of the mouse transcriptome based on functional annotation	
of 60,770 full-length cDNAs	
Nature 420, 563-573 (2002)	
6 (bases 1 to 2056)	
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,	
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,	
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,	
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,	
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,	
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,	
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,	
Okazaki, Y., Saito, R., Shibata, K., Sakai, C., Sakai, K., Sakazume, N.,	
Sano, H., Saeki, D., Shimada, K., Shinagawa, A., Shiraki, T.,	
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,	
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,	
Muramatsu, M. and Hayashizaki, Y.	
Direct Submission	
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of	
Physical and Chemical Research (RIKEN), Laboratory for Genome	
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,	
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,	
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,	
Fax: 81-45-503-9216)	
cDNA library was prepared and sequenced in Mouse Genome	
Encyclopedia Project of Genome Exploration Research Group in Riken	
Genomic Sciences Center and Genome Science Laboratory in RIKEN.	
Division of Experimental Animal Research in Riken contributed to	
prepare mouse tissues.	
Please visit our web site for further details.	
URL: http://genome.gsc.riken.jp/	
URL: http://fantom.gsc.riken.jp/	
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DB 62 GAATGGCTCAACTAAATGGGCTTATAAATGGTGAAGGCAACAAGTATCTCGGATGCTTTT 121	
QY 1196 ATTGGGCGAGTTCGAACCTTTAAATACCAATGTCGGCTTCAGAACACAACTTTATTG 1255	
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DB 182 AAATGTTTTTCAACTCTTGAAATTTTTTTTCTGAGTTTTTGTCTCCAGCTTAATTG 241	
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/clone_lib="RIKEN full-length enriched mouse cDNA library"	
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(MGD MG1:1353562, GB NM_013927, evidence: BLASTN, 100%,	
match=2055)"	
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Query Match 33.6%; Score 815.8; DB 3; Length 2056;	
Best Local Similarity 77.5%; Pred. No. 6.2e-179;	
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LOCUS          bxl6c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
DEFINITION     sapiens cDNA clone bxl6c03 5', mRNA sequence.
ACCESSION      BF725470
VERSION        BF725470.1 GI:12041381
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 553)
Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
NEIBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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BX"
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tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript plasmid system
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTTCTTATGATCGGCGGCCGCC(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."
ORIGIN
Query Match      22.8%; Score 553; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 8.7e-118;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 541 ATCCGTTCTCTAT 553

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LOCUS          DKFZp686A1695.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION     DKFZp686A1695 5', mRNA sequence.
ACCESSION      AL713036
VERSION        AL713036.1 GI:19696392
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
Bloeker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
Wiemann,S.
EST (Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp686A1695) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686A1695"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="686 (synonym: hlcc3)"
/note="vector: pTriplex2; Site 1: SfiIA; Site 2: SfiIB;
cDNA-collection"
ORIGIN
Query Match      19.7%; Score 478; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.6e-100;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGTTTAAATCGCTGACAAAAGTCACAAAGTGAAGCTTATAGGAGAGAACCAATGAGAA 60
Db 50 ATGTTTAAATCGCTGACAAAAGTCACAAAGTGAAGCTTATAGGAGAGAACCAATGAGAA 109
QY 61 GAACAAAGTTCTCGTCGGAATGAAGAGGCTCTCACCCAAAGTAATCAGTCTCAGCAAAAC 120
Db 110 GAACAAAGTTCTCGTCGGAATGAAGAGGCTCTCACCCAAAGTAATCAGTCTCAGCAAAAC 169
QY 121 ACAGCACAGGAGAGAAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCAGTTC 180
Db 170 ACAGCACAGGAGAGAAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCAGTTC 229
QY 181 ACCTCTGAAGAGGACACACACACACATACAGAGAAATCTCTCAAGAGAAATCTCTCTGGA 240
Db 230 ACCTCTGAAGAGGACACACACACACATACAGAGAAATCTCTCAAGAGAAATCTCTCTGGA 289
QY 241 GATCTGACCAAAACCTGACCTCAAAATGCAGCAGAACCAACTGGAACAGTGCACAGAG 300
Db 290 GATCTGACCAAAACCTGACCTCAAAATGCAGCAGAACCAACTGGAACAGTGCACAGAG 349
QY 301 CAGAAGAAATGACACCCCGGGAAGAGGTCCAAAACAGCCCAAAACCAACCCGCTGCA 360
Db 350 CAGAAGAAATGACACCCCGGGAAGAGGTCCAAAACAGCCCAAAACCAACCCGCTGCA 409
QY 361 GCTCTGTTTAAATGAGTATGCGATGCCAGTCCAGTACACAACTGGTGAAAAGAAATGCGT 420
Db 410 GCTCTGTTTAAATGAGTATGCGATGCCAGTCCAGTACACAACTGGTGAAAAGAAATGCGT 469
QY 421 CAAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAAG 478
Db 470 CAAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAAG 527

RESULT 4
LOCUS CR626336
DEFINITION full-length cDNA clone CS0DK009YE13 of HeLa cells Cot 25-normalized
of Homo sapiens (human) .
ACCESSION CR626336
VERSION 1 GI:50507143
KEYWORDS HTc; cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1947)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .1947
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK009YE13"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

FEATURES
source
ORIGIN
1
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1820
GTCGCTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGCTCGAACTGCCAA
1820
ATCTGTTTGGAGAAATAGCTTGTGCTGTGTGGGGGGGAAACCGGGCGACCGCCAA 963
TGTGGTGGCCGACGGGTTTGCCAAATCTTTAACTCTAGACAAAAGACCTCGAAAT
1880
CGTGGTGGCGACGGGTTTACCAACCTCTTCATCTGGATAGAGAGACCTGTAATGAGAT
1023
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Query Match
Best Local Similarity 19.6%; Score 477.4; DB 3; Length 1947;
Matches 712; Conservative 0; Mismatches 391; Indels 0; Gaps 0;
QY 861 AAATGAGCTAAGGAAACACTCAGGACTTCTTCAAAAATTTTCAAGTTGGATGTCGATCAAT 920
Db 4 AAAGGACATGCGAAATAACTACTGAGTCTCGCGCTTCAAGATGGAGCTCTCAGCCT 63
QY 921 AATACATTTGATATTTGCTACTCTTCTTTGGGTTTAAATCCAAATGTTTAGAGCAAAATAG 980
Db 64 CTTGCCCTTGGATTTTCTTATTTGAAAGTCGGTGTGAACCCCTCTCCTCGGCTGCCCG 123
QY 981 GATGTTAAAGTACACTTTCATTTTGAATTTTAAATCATCACCTTAGAGTCTTATTAATGGACAA 1040
Db 124 CTGTTTAAAGTACATGGCTCTCTCGAGTTTAAACAGCGCTTGAATCCATCCTCAGCAA 183
QY 1041 AGCATATATCTACAGAGTTATTCGAACAACTGGATACTTGTGTTTATTTCTGCACATTA 1100
Db 184 AGCTACGTGTACAGGGTTCATCAGGACCAACAGCTTCTCTACAGCTCGATTTGAA 243
QY 1101 TGCCTGTGTTTATTACTGGCTTCAAACTATGAAGAAATTTGGCACTTACTAGATGGGTGA 1160
Db 244 TTCCTGTCTTTATTTACTGGGATCGGCTATCAGGGCTCGGCTCCACTCCTGSGTTTA 303
QY 1161 TGATGGGGAAGAAACGAGTATCTGAGATGTTTATTTATTTGGGAGTTTCGAACTTTAAATAC 1220
Db 304 CGATGCGGTGGGAAACAGTTTATTTCCGTGTTTACTTCTGCTGTGAAGACCTCATCAC 363
QY 1221 CATTTGGTGCCTTTCAGAAACCAAACTTTATTTGAAATTTTTCACCTCTTGAATTT 1280
Db 364 CATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTCTGAAATTA 423
QY 1281 TTTTCTGAGATTTTGTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGTGATTTGGAGC 1340
Db 424 TTTTACGGGCTTTTGTGTTCTCTGTGATGATCGGACAGATGAGAGATGTGTTAGGGC 483
QY 1341 AGCTACAGCAATCAGAACTACTTCCGGCTTGCATGAGATGACACATTGCTTACATGAA 1400
Db 484 CGCCACCGCGGACAGACCTACTACCGGAGCTGCTATGGACAGCAGCGTGAAGTACATGAA 543
QY 1401 CAATTTACTCATTTCTTAACTTTGCAAAAGCGAGTTTCGAGCTTGTATGAATATATATG 1460
Db 544 TTTCTACAAGATCCCAAGTCCGTCAGAACCGGTCGAAGACCTGGTAGAGTACACCTG 603
QY 1461 GGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGACCTTACCAACTACGTTCCA 1520
Db 604 GCATCGCAAGCATGCTGGATGAGTACAGCTGATGGTGCAGCTTCCAGACAAGATGCG 663
QY 1521 GTTAGCCCTCGCCATTGATGTGAATTTACAGATCATCAGCAAGTGCATTTGTTCAAGGG 1580
Db 664 GCTGGACCTCGCCATCGAGTGAACTTACAACATCGTTAGCAAAAGTCGCACTCTTTTCAGGG 723
QY 1581 TTTGTATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCGTTCTCTTATTTGCC 1640
Db 724 CTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGTCTACCTGCC 783
QY 1641 TGGTGACTTTGCTGCAAAAAGGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGG 1700
Db 784 CAACGACTATGTGCAAGAGGGGAGATCGGCGGTGAGATGTATCATCCTCAGGAGG 843
QY 1701 AGAAGTCCAAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTTACTTCTGAAAGCTGG 1760
Db 844 GCAAGTGCAGGTCTTGGGGGGCTCTGATGGGAAATCTGTGCTGGTACGCTGAAAGCTGG 903
QY 1761 GTCGCTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGCTCGAACTGCCAA 1820
Db 904 ATCTGTTTGGAGAAATAGCTTGTGCTGTGTGGGGGGGAAACCGGGCGACCGCCAA 963
QY 1821 TGTGGTGGCCGACGGGTTTGCCAAATCTTTAACTCTAGACAAAAGACCTCGAAAT 1880
Db 964 CGTGGTGGCGACGGGTTTACCAACCTCTTCATCTGGATAGAGAGACCTGTAATGAGAT 1023
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DEFINITION bx16c03.x1 Human Iris cdna (Un-normalized, unamplified): BX Homo sapiens cdna clone bx16c03 3', mRNA sequence.

ACCESSION BF725469

VERSION BF725469.1 GI:12041380

KEYWORDS EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 437)

AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.

TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics

JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press

COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="bx16c03"
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/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cdna (Un-normalized, unamplified): BX"
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cdna library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adapted
[5'-pGACTAGTTCTAGATCGGCGCGGCC(7)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 17.7%; Score 430.2; DB 2; Length 437;
Best Local Similarity 99.3%; Pred. No. 3.5e-89;
Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1759 GGCTCGGTGTTTGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTGCC 1818

DB 437 GGCTCGGTGTTTGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTGCC 378

QY 1819 AATGTGTGCCCCACGGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTCCAGAA 1878

DB 377 AATGTGTGCCCCACGGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTCCAGAA 318

QY 1879 ATTCTAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAGAGTGCCTTTA 1938

DB 317 ATTCTAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAGAGTGCCTTTA 258

QY 1939 AAGCAGAGGCTAAGACCGCAGAAAGCAACCCCTCCAGAAAGAGATCTTGCCTCTCTTC 1998

DB 257 AAGCAGAGGCTAAGACCGCAGAAAGCAACCCCTCCAGAAAGAGATCTTGCCTCTCTTC 198

QY 1999 CCACCGAAGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCACAGAAAGCA 2058

DB 197 CCACCGAAGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCACAGAAAGCA 138

QY 2059 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAGAAAAGAAAATTCT 2118

DB 137 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAGAAAAGAAAATTCT 78

QY 2119 GAAGGAGGAG 2178

DB 77 GAAGGAGGAG 18

QY 2179 CAAAAAGAGAAATGAA 2193

DB 17 CAAAAAGAGAAATGAA 3

RESULT 7

LOCUS BE287002

DEFINITION 601097229F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:3496015 5', mRNA sequence.

ACCESSION BE287002

VERSION BE287002.1 GI:9165707

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 881)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM8547 row: i column: 08
High quality sequence stop: 774.
Location/Qualifiers
1. 881
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3496015"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
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/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

FEATURES

source

Query Match 16.6%; Score 402.4; DB 2; Length 881;
Best Local Similarity 73.9%; Pred. No. 1.2e-82;
Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;

QY 1459 TGGGACTCTCAAGAGATGCTAGATGATGCTTTTAAAGACCTCACCACCTACGGTC 1518

DB 1 TGGAACTCAAGAGATGCTAGATGATGCTTTTAAAGACCTCACCACCTCAGAGAGATG 60

QY 1519 CAGTTAGCCCTCGCCATTGATGTGAACCTTCAAGATCATCAGCAAGTCAAGTTGTTCAAG 1578

DB 61 CAGTTGTCTATTGCCCCCTTGACATAACTTCAGTATCATCCAAAGGTGGAGTTATTCAAG 120

QY 1579 GGTGTGTATACAGATGATTTTATGACATGTTGCTTAAGATTGAATCCGTTCTCTATTG 1638

Db 121 GCGTGTGACACAGATGATTATGACCTGCTGAAGATTGAATCCACTATTATTTA 180
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Db 181 CCTGTGTACTTTGTCTGCAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAACAC 240
Qy 1699 GGAGAGTCCAGTTCCTGGAGCCCTGATGTGTAAGTTCTGGTACTCTGAAAGCT 1758
Db 241 GGAGAGTCCAGTTCCTGGAGCCCTGATGTGTCCTCAAGTTCTGGTACTCTGAAAGCT 300
Qy 1759 GGGTCGGTGTGTTGGAGAAATCATGACCTCTTAGCAGCAGGAGGAGAAACCGTGCAGTGC 1818
Db 301 G-----GCCCTTCTGGCAAAAGGAGGAGAAATCGCCGACAGCT 339
Qy 1819 AATGTGTGGCCCAAGGTTGGCAATCTTTAACTCTAGACAAAGAACCTTCCAGAA 1878
Db 340 GATGTGTGGCCCAAGGTTGGCAATCTTTAACTCTAGACAAAGAACCTTCCAGAA 399
Qy 1879 ATTCTAGTGCATTATCCAGATCTCGAAGGATCCTCATGAGAAAGCCAGAGTGTCTTTA 1938
Db 400 ATTCTGTGCTATTATCCAACTCTTAAAGCTCTCATGAGAAAGCCAAATTCCTTTA 459
Qy 1939 AAGCAGAGGCTTAAGACCGCAGAACCAACCCCTCCAGAGAAAGATCTTGGCCCTCTCTTC 1998
Db 460 AGCCAGAGGAGAAAGCACTCAGCAATCCCTGCAAGACCGAGGACCTGCTTCTTTTC 519
Qy 1999 CCACGAAAGAGAGACACCCAACTGTTTAAACTCTCTAGGAGGACAGGAGAAAGCA 2058
Db 520 CCACGAAAGAGAGACACCCGATGCTTAAAGTTCTCTTAGGACACACAGGAGGTTG 579
Qy 2059 AGCTTGTGCAAGTACTCAATTTGAAGCGAGGAGCAAGCAAGTCTAG--AAGAAAGAAAT 2116
Db 580 ACCTTGTGAAGACTCTCTTAAGGAAAGAGAAAGAAACCAACCTCAGAAATAACCGTGAA 639
Qy 2117 CTGAAGGAGGAGAGAGAGAGAGAAAGAAATGAAGATAAAGAAAGAAATGAAGATA 2176
Db 640 GTTCACAGGAGCTT 699
Qy 2177 AACAAAAAGAAATGAAGATA 2198
Db 700 AGCAGAAAAAGAGAGAAAAA 721

RESULT 8

BX401127
LOCUS BX401127 1054 bp mRNA linear EST 28-APR-2004
DEFINITION BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CSODK009YE13 5-PRIME, mRNA sequence.
ACCESSION BX401127
VERSION BX401127.2 GI:46846684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1054)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30614460.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7817.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSODK009AC07QPi&c=7817.r.
Location/Qualifiers

FEATURES

source

1. .1054
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK009YE13"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 15.0%; Score 363.8; DB 5; Length 1054;
Best Local Similarity 60.8%; Pred. No. 1.2e-73;
Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;
Qy 861 AAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGCGCATCAAT 920
Db 4 AAAGGATATGCAATAACTACCTGAGTCTCGCGCTTCAAGATGGACCTGCTCAGCCT 63
Qy 921 AATACCAATTTTCATATTTGCTACTCTTCTTTGGGTTTAAATCCAATGTTTAGAGCAAAATAG 980
Db 64 CTTGCCCTTGGATTTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCCCGCTGCMCG 123
Qy 981 GATGTTAAA--GTACACTTTCATTTTTTGAATTTTAAATCATCACCTAGAGTCTATAATGGAC 1038
Db 124 CTGTTTAAATGTATCATGGCCCTTCTCGAGTTTAAACGCCGCTGGATTCATCTCTCAGC 183
Qy 1039 AAAGCATATATCTACAGAGTTTATTGAAACAACTGGATACTTGTGTTTATTCTGCACAT 1098
Db 184 AAAGCTACGTGTACAGGTCATCAGGAYCACAGYTTACCTTCTVTACAGCTGCTATTG 243
Qy 1099 AATCGCTGTGTTTATTACTGGGCTTCAAATATGAAGAAATTTGGCACTACTAGATGGTG 1158
Db 244 AATTCTGTCTTTTATTACTGGGCATCGGCTTCAAGGCTCTCGGCTCCACTCACTGGGTT 303
Qy 1159 TATCATGGGAGGAAAGAGTATCTGAGATGTTTATTATTGGGAGTTTCGAACCTTTAAT 1218
Db 304 TACGATGGGTGGGAAACAGTTTATTTCGCTGTGTACTCTTGTGTGAARACMCTCATC 363
Qy 1219 ACCATTGGTGGCTTCCAGAACCAAACTTTATTGAAATTTGTTTTCAACTCTTGAAT 1278
Db 364 AYCATCGGGGGCTGCTGACCCCAAGAYACTTTTGAAATTTGTTTCCAGCTGTGTAAT 423
Qy 1279 TTTTTCCTGAGGTTTGTGTTCTCCAGTTTAAATGGTTCAGATGAGAGATGTTGGA 1338
Db 424 TATTTACGGGCGTCTTTTGTCTCTGTGATGATTGGACAGATGAKAGATGTGTTAGGG 483
Qy 1339 GCAGCTACAGCAATCAGAACTACTTCCGCGCTGATGATGATGATGATGATGATGATGATG 1398
Db 484 GCCGCCACCG--CAGACAGACCTTACTACCGAGCTGTCATGGAGCAGCAGCGTGAATGATG 542
Qy 1399 AACAAATTAATCTCCATTCTTAACTTTGTGCAAAAGCGAGTTCCGAGCTTGGTATGAATATACA 1458
Db 543 AATTTCACAGATCCCAAGTCCGTCGAGAACGAGTCAAGACTGTTGTAAGATGATACACC 602
Qy 1459 TGGAGCTCTCAAGAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1518
Db 603 TGGCACTCGCAAGGCATGCTGGATGATGATGATGATGATGATGATGATGATGATGATG 662
Qy 1519 CAGTTAGCCCTCGCCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1578
Db 663 CGGTGAGCTTCGCCATTCGACATGAATACAACTGTTAGCAAAAGTTCGCACTCTTTTTCAG 722
Qy 1579 GGTGTGATACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1638
Db 723 GGCTGTACCCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
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QY 1430 ACCGAGTTGGGACTTGGTATGATATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTG 1489
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 QY 1490 ATTTGCTTAAGACCTACCACTAGCTGGTCCAGTTAGCTTCCCTCCCTCCCTGAACTTCA 1549
 Db 241 AGCTGATGGTCAAGCTTCCAGCAAGATGCGGCTGGACCTCGCCATCGACCTGAACTACT 300
 QY 1550 GCATCATCAGCAAGTCCGACTTGTTCAGGGTGTGTATACACAGATGATTTATGACATGT 1609
 Db 301 ACATCGTTAGCAAGTCCGACTTTCAGGGTGTGTACCGGCAAGTATCTTTGACATGC 360
 QY 1610 TGCTAAGATTGAATCCGTTCTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669
 Db 361 TGAAGAGCTTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 1670 TTGGCAAGAAATGATATATCATCATGATGAGGATGAGGATGAGGATGAGGATGAGG 1729
 Db 421 TCGGCGGTGAGTATCATCATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 480
 QY 1730 GTACTAAAGTTCGTTACTCTGAAAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1789
 Db 481 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 1790 CAGCAGGAGGAGAAACCGTCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1849
 Db 541 CTGTTGGGGGGGAAACCGGCGCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 1850 TAACTCTAGACAAAGAACCTCCAG--AAATTCAGTGCATATTCAGATTCGA 1904
 Db 601 TCATCCTGGATGAAGAGGACCTGAATGAAATTTTGGTGCATATTCCTGAGTCTCA 656

RESULT 11
 BQ068992
 LOCUS
 DEFINITION BQ068992 978 bp mRNA linear EST 02-APR-2002
 AGENCOURT 6740166 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802872
 5', mRNA sequence.
 BQ068992
 VERSION BQ068992.1 GI:19898038
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 978)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2037 row: p column: 09
 High quality sequence stop: 726.
 Location/Qualifiers
 1. 978
 /organism="Homo sapiens"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_47"
 /note="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'

FEATURES

source
 CK619966 633 bp mRNA linear EST 26-JAN-2004
 LOCUS mk30e03.y1 Mouse retina, unamplified: mk/ml Mus musculus cDNA clone
 DEFINITION mk30e03.5', mRNA sequence.
 CK619966
 ACCESSION CK619966.1 GI:41340852
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 633)
 Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
 Buchoff,P., Wistow,G. and Hjelmeland,L.
 Expressed sequence tag analysis of mouse retina
 TITLE

adaptor: GGCACGAG (G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.7%; Score 308.4; DB 5; Length 978;
 Best Local Similarity 67.7%; Pred. No. 9.9e-61;
 Matches 432; Conservative 0; Mismatches 206; Indels 0; Gaps 0;
 QY 1326 AGATGTGATGGAGAGCTACAGCAATCAGAACTACTTCCGCTGCATGGATGACAC 1385
 Db 1 AGATGTGATGGAGAGCTACAGCAATCAGAACTACTTCCGCTGCATGGATGACAC 60
 QY 1386 CATTGCCCTACATGAACAACTTACTCCATCTTCAAGATGCTGCAAGAGCGGCTCAAGACCTG 1445
 Db 61 GGTGAAGTACATGAATTTTCAAGATGCTGCAAGAGCGGCTCAAGACCTG 120
 QY 1446 GTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTTAAGACCT 1505
 Db 121 GTACGAGTACACCTGGCACTCGCAAGGATGCTGATGAGTCAAGCTGATGGTGCAGCT 180
 QY 1506 ACCAACTACCGTCCAGTTAGCCCTCGCCATTTGATGTGAACCTTCAGCATCATCAGCAAA 1565
 Db 181 TCCAGACAGATGCGGCTGGACCTCGCATCGAGTGAACCTTACCAATCGTTAGCAAA 240
 QY 1566 CGACTTGTTCAGGGTGTGTATACAGATGATTTATGACATGTTGCTTAAGTTGAATC 1625
 Db 241 CGCACTCTTTACGGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTC 300
 QY 1626 CGTTCTCTATTGCTGCTGACTTTGCTGCAAAAGGAGAAATTCGCAAGGAAATCTA 1685
 Db 301 TGTGCTTACTGCTGCCACGACTATGTGCAAGAGGGGAGATCGGCCGTGAGATGTA 360
 QY 1686 TATCATCAAGCATGGAGAAAGTCCAAAGTTCCTTGGAGGCCCTGATGCTACTAAAGTTCTGGT 1745
 Db 361 CATCATCCAGGAGGCAAGTGCAGGCTTTGGGCGGCCCTCATGGGAAATCTGTGCTGGT 420
 QY 1746 TACTCTGAAGCTGGTTCGGTGTGAGAAATCAGCTTCTAGCAGCAGGAGGAGAA 1805
 Db 421 GACGCTGAAGCTGGATCTGTGTTTGGAGAAATTAAGCTTGTGCTGTGTTGGGCGGGAA 480
 QY 1806 CCGTGCAGAACTGCCAATGCTGGTGGCCACCGGTTTCCCAATCTTTTAACTCTAGACAAAA 1865
 Db 481 CCGCGGACGCGCCAACTGTTGGGCGCACGGGTTTACCACCTCTTCTCTCTGGATAGAA 540
 QY 1866 GACCTCTCAAGAAATCTAGTGCATTTCCAGATTTCTGAAAGGATCTCTCATGAAGAAAGC 1925
 Db 541 GGACCTCAATGAGATTTTGGTGCATTTATCTGAGTCTCAGAAAGTTACTCCGGAAGAAAGC 600
 QY 1926 CAGAGTCTTTTAAAGCAGAGGCTTAAGCGCGAGAAG 1963
 Db 601 CAGCGCATCTCTGAGAGCAACCAATAAGCCCAAGGAGG 638

RESULT 12

CK619966
 LOCUS
 DEFINITION CK619966 633 bp mRNA linear EST 26-JAN-2004
 mk30e03.y1 Mouse retina, unamplified: mk/ml Mus musculus cDNA clone
 DEFINITION mk30e03.5', mRNA sequence.
 CK619966
 ACCESSION CK619966.1 GI:41340852
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 633)
 Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
 Buchoff,P., Wistow,G. and Hjelmeland,L.
 Expressed sequence tag analysis of mouse retina
 TITLE

JOURNAL
COMMENT

Unpublished (2004)
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 30 row: e column: 03
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .633
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL6J"
/db_xref="taxon:10090"
/clone="mk30803"
/sex="Male"
/tissue_type="retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Mouse retina, unamplified: mk/ml"
/notes="Organ: Eye; Vector: pSPORT1; 270ug total RNA was extracted from 200 adult male mouse retinas. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGAGTGTCTAGATCGGAGCGGCCGCTTT-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 12.5%; Score 304; DB 7; Length 633;
Best Local Similarity 67.6%; Pred. No. 9.7e-60;
Matches 427; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1315 GGTGAGATGAGATGTGATGAGAGCTGACGACCAATCAGAACTACTTCCGGCGCTGC 1374
DB 1 GGACAGATGAGATGTGTGGGGCGCCACAGCGGGGACGACCTACTACCGAGCTGC 60

QY 1375 ATGATGACACCATTCCTACATGCAAAATTAATCTCCATTCCTAACTTGTGCAAAAGCGA 1434
DB 61 ATGGACAGCAGATGAGTACATGAATCTTCAAGATCCCGAGGTCTGTGCGAAGCCGT 120

QY 1435 GTTCGACCTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTGG 1494
DB 121 GTCAAGACCTGGTATGAGTACACTTGGCATTCGCAAGGCATGCTGGATGAGTCAGAGCTG 180

QY 1495 CTTAAGACCTACAACTACGCTCCAGTTAGCCCTCGCCATTCAGTGAATTCAGATC 1554
DB 181 ATGATACAACTTCGGACAAAGATGCGACTGGACCTGGCCATTGATGTGAATACAGTATT 240

QY 1555 ATCAGCAAGTCAGCTGTTCAAGGTTGTGATACACAGATGATTATGACATGTTGCTA 1614
DB 241 GTCAGCAAGTGGCCCTCTTTCAGGGGCTGTGACCGGCAGATGATTCGACATGCTCAAG 300

QY 1615 AGATTGAAATCCGTTCTCTATTTCCTGTGTGACTTTGTCTGCAAAAGGAGAAATTTGGC 1674
DB 301 CGGCTTCGTTCTGTCTACCTACCCCAATGACTATGTGTGCAAGGGGAGATTGGC 360

QY 1675 AAGCAATGATATCATCAAGCATGAGAGAGTCCAAAGTCTTCGAGGCCCTGTAGTACT 1734
DB 361 CGAGATGATACATATCCAGGGCGGGGAGTGCAGGTGCTGGCGGCCCGCCAGATGGGAAG 420

QY 1735 AAGTTCTGTTACTCTGAAGCTGGTGGTGTGTTGGAGAAATCAGCTTCTAGCAGCA 1794
DB 421 GCTGTGTTGATCAATCAAGCCGGATCGGTGTTTGGAGAAATAGATTGCTGCTGTC 480

QY 1795 GGAGGAGGAAACCGTCGAATGTGGTGGCCCGCCAGGGTTTCCCAATCTTTTAACT 1854
DB 481 GGGGTGGCAACCGCGCGCACAGCAAGTGTGGCCCATGGCTTCCACCACTCTTCATA 540

QY 1855 CTAGACAAAGAACCTCCCAAGAAATTCCTAGTGCATTATCCAGATTCTGAAAGATCCTC 1914
DB 541 CTGGCAAGAAGGACTTGAATGAAATTTTAGTGCATTACCGGAATCTCAGAGTTACTT 600

QY 1915 ATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAA 1946
DB 601 CGAAGAGCCAGCGGCGCATGCTAAGAAATAA 632

RESULT 13
AUI37778

LOCUS AUI37778 PLACE1 Homo sapiens cDNA clone PLACE1007225 5', mRNA
DEFINITION sequence.
ACCESSION AUI37778 694 bp mRNA linear EST 02-AUG-2002
VERSION AUI37778
KEYWORDS AUI37778.1 GI:10999299
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 694)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isoigai, I.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
Location/Qualifiers
1. .694
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/clone="PLACE1007225"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 12.4%; Score 301.4; DB 1; Length 694;
Best Local Similarity 66.3%; Pred. No. 4e-59;
Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;

QY 1049 TCTACAGAGTTATTCGAACAACCTGGATACCTGCTTTTATTCGCACATTAATGCTGTG 1108
DB 20 TCTGCAAGGTCTATCAGGACCAAGCCCTACCTTCTCTACAGCTGCAATTTGAATTCCTGTC 79

QY 1109 TTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGG 1168
DB 80 TTTATTACTGGGCATCGGCTATCAGGGCTCGGCTCCACTCAGTGGGTTTACGATGGCG 139

QY 1169 AAGGAAACAGATCTGAGATGTTATTTATTTGGGAGTTCGAACCTTTAATACATTTGGTG 1228
DB 140 TGGGAAACAGTTATATTCGCTGTACTTCTGTGTGTAAGACCCCTCATCACCATCGGGG 199

QY 1229 GCCTTCCGAACCAACAACTTTTATTGAAATGTTTTTCAACTCTTGAATTTTTTTTCTG 1288
DB 200 GGCTGCTGACCCCAAGACACTCTTTTGAATTTGTTCTTCAGCTGCTGAATTTATTCACGG 259


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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match      11.6%; Score 280.8; DB 4; Length 738;
Best Local Similarity 63.0%; Pred. No. 2.6e-54;
Matches 466; Conservative 0; Mismatches 272; Indels 2; Gaps 2;

QY 748 ATACACTACTGGCTTATTGGGACATCATATGTGATATCATCTTACCTTTATGATATGCTA 807
DB 1 ATCCACTTCTGGCTCCTCATGGATTACTTGTGGACTTCATCTACCTCCTGGACATCACC 60

QY 808 TTATTCAGCCAGACTCCAGTTTGTAAAGAGGAGGACATAAATAGTGGATTCAAAATGAG 867
DB 61 GTGTTCCAGATGCGCTGCAG-TTGTCAAAGGGGGGACATCATTAACAGACAAGAGGAG 119

QY 868 CTAAGGAAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTCGCATCAATAATACCA 927
DB 120 ATGCGTAATAACTACCTGAAAGTCTCGCCGGTTTAAAGATGGACCTGCTCTGCCCTCCTGCC 179

QY 928 TTTGATATTGCTACCTCTTCTTTGGGTTTAAATCCAATGTTTAGAGCAATAGATGTTA 987
DB 180 TTGGACTTCTCTACTTGAACCTTGGCATCAACCTCTCCTTCGCTGCCCGCTGCTG 239

QY 988 AAGTACACTTCATTTTTGAATTAATCATCACTAGAGTCTATAATGGAACAAAGCATAT 1047
DB 240 AAGTACATGCGCTTCTTTGAGTTTAAATAACCGCTCGAAGCCATCCTCAGCAAAAGCCTAC 299

QY 1048 ATCTACAGAGTTATTCGAAACACTGGATCTTCTGCTTTTATTCTGCACATTAATGCTGT 1107
DB 300 GTTTACAGAGTATCAGGACCGGCTTCTGCTGTACAGCCCTGCACCTCAACTCCTGC 359

QY 1108 GTTTATTACTGGGCTTCAAACCTATGAAGAAATGGCACTACTAGATGGGTGATGATGG 1167
DB 360 CTTTACTACTGGGATCAGCCT-TCCAGGATCGGCTCCACTCAGTGGGTTTACGACGGA 418

QY 1168 GAAGGAAACGAGTATCTGAGATGTTATTATTGGGAGTTTCGAACTTTAATTACCATGGT 1227
DB 419 GTGGGAAACAGTTATATTCGATGCTACTACTGGGCTGTGAAACCCCTCATCACCATCGGA 478

QY 1228 GGCCTTCCAGAACACAACTTTATTGAAATGTTTTCAACTCTTGAATTTTTTTCT 1287
DB 479 GGACTGCCCGACCCCGACGCTCTTTGAGATTGTCTTCAGCTGTGAACTATTTTACC 538

QY 1288 GGAGTTTTTGTCTTCTCCAGTTTAAATGGTCAGATGAGAGATGTGATTGGAGCAGCTACA 1347
DB 539 GGGGTCTTTGCTTCTCTGTGATGATTGGACAGATGAGAGATGTGTGGGGGCGGCCACA 598

QY 1348 GCCAATCAGAACTACTTCGCGGCTGCATCGATGACACCACTTGCCTACATGAACAATTAC 1407
DB 599 GCGGGGACAGACCTACTACCGCAGCTGCATGGACAGCAGTGAAGTACATGAATCTCTAC 658

QY 1408 TCCATTCTTAACTTGTGCAAAAGCGAGTTTCGACTTGGTATGAATATACATCGGACTCT 1467
DB 659 AAGATCCCCAGGCTGTGCGAAGACCGGTGTCAAGACCTGGTATGAGTACACCTGGCATTCG 718

QY 1468 CAAAGAAATGCTAGATGAGTC 1487
DB 719 CAAGGCATGCTGGATGATC 738
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Search completed: March 27, 2005, 18:01:24
Job time : 7059 secs